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Sequence 9, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 5741, Ap
Sequence 12702, A
Sequence 12702, A
Sequence 12812, A
Sequence 8043, Appl
Sequence 8043, Appl
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Sequence 8301, Ap
Sequence 5419, Ap
Sequence 12563, Appl
Sequence 32, Appl
Sequence 62, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
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11, Appl
16, Appl
16, Appl
7691, Ap
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TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REFERENCE: 68126891209900
CURRENT APPLICATION NUMBER: US/09/870,089B
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1296, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA101
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100.0%; Pred. No. 6.1e+05;
tive 0; Mismatches 0;
US-09-895-072-15
US-09-986-552-15
US-10-024-197-9
US-10-024-197-9
US-10-023-889-9
US-10-023-889-9
US-10-023-889-9
US-10-023-889-9
US-10-023-889-9
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US-09-815-242-12702
US-09-815-242-12702
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US-09-815-242-12543
US-09-815-242-12543
US-09-815-242-12563
US-10-10-627-62
US-10-10-121-18
US-10-10-10-121-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 13, Application US/09870089B; Publication No. US20030175252A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: ATF4/CREB-2 US-09-870-089B-13
  Query Match
Best Local Similarity 10u...
Pre 9; Conservative
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                            RESULT 2
US-09-925-300-1296
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  TYPE: PRT
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Sequence 252, Appl
Sequence 8, Appli
Sequence 10, Appl
Sequence 47039, A
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2, Appli
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Sequence 89, Appl
Sequence 14, Appl
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                                                                                                 2003, 14:18:11; Search time 22:1667 Seconds (without alignments) 75.512 Million cell updates/sec
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Sequence
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18: /cgm2_6/ptcdata/2/pubpaa/US10A_PUBCOMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-925-300-1296 ·· US-09-925-300-1296 ·· US-09-882-27-252

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US-09-882-27-252

US-10-116-788A-10

US-09-864-761-47039

US-09-864-761-47039

US-09-815-242-10094

US-09-815-242-10094

US-09-815-242-10094

US-09-815-242-10094

US-09-815-242-10094

US-09-815-242-10094

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US-10-228-073-2
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 KHFKPHGFS 9
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Match Length
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78.2
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63.6
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Maximum DB seq
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78.2%; Score 43; DB 12; Length 348;
Best Local Similarity 87.5%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 1; Indels
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Pred. No. 0.074;
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JAPRICANT: MARAILON
JAPRICANT: Larson, Marilyn A.
JAPRICANT: Larson, Marilyn A.
JAPRICANT: Meber, Annika
TITLE OF INVENTION: Genomic Mammary Amyloid A Sequence
FILE REFERENCE: P04557031
CURRENT APPLICATION NUMBER: US/10/116,788A
CURRENT FILING DATE: 2002-06-10
PRIOR PILING DATE: 2002-06-10
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
SPIOR FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
Best Local Similarity 100.0%; Pred. No. 0.0.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID 0252
LENOTH: 348
                                                                                                                                                                                                                                             ; Sequence 252, Application US/09882227; Publication No. US20030158396A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10116788A; Publication No. US20030170840A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Equus caballus
                                                                                                                             42 KHFKPHGFS 50
                                                                                       1 KHFKPHGFS 9
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TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US 10/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR PILING DATE: 2002-01-15
PRIOR PLING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
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TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REFERENCE: 6812681209900
CURRENT APPLICATION NUMBER: US/09/870,089B
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTAME: FastSEQ for Windows Version 3.0
               CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR PELING DATE: 2000-03-08
PRIOR PELING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SENGTH: 286
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; Sequence 67, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 67
LENGTH: 351
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ORGANISM: Homo sapiens
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S-09-925-300-1296
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Matches 9; Conserva
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US-09-870-089B-2
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APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miler, Charles
APPLICANT: Miler, Charles
APPLICANT: Miler, Charles
APPLICANT: Ocomen, Farmonois
APPLICANT: Ocomen, Farmonois
APPLICANT: Ocomen, Farmonois
TITLE OF INVENTION: Encoding No. US20030158396Alel Helicobacter Polypeptides in the FITILE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/082,227
CURRENT FILING DATE: 100-06-15
PRIOR FILING DATE: 1097-07-29
PRIOR FILING DATE: 1997-07-29
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ORGANISM: Homo sapiens
FRAUTURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.52
OTHER INFORMATION: EXPRESSED IN ADUIT LIVER, SIGNAL = 0.58
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EST HUMAN HIT: Q16515, EVALUE 2.00e-25
OTHER INFORMATION: SWISSPROT HIT: Q16515, EVALUE 2.00e-51
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APPLICANT: 29skind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Carri J.
APPLICANT: Carri J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REPERBNCE: ELITRA.011A
                                                   FRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PRIING DATE: 2000-09-21
PRIOR PRIING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-29
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 47039
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Pred. No. 66;
1; Mismatches
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CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/259,331
PRIOR APPLICATION NUMBER: 60/269,336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10094, Application US/09815242
Patent No. USZ0020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 63.6%;
Similarity 66.7%;
6; Conservative 1
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50 KHYKPKQFS 58
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Matches 6; Conserv
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APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
ITILE OP INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OP INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE OP INVENTION: HUMBER: US 60/180, 312
FILE REPERENCE: Acomica-X-1
CURRENT FILING DATE: 2000-02-04
FRIOR PAPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-03
PRIOR PAPLICATION NUMBER: US 60/207, 456
PRIOR PILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
PRIOR PILING DATE: 2001-09-07
PRIOR PILING DATE: 2001-09-07
PRIOR PILING DATE: 2001-00-07
PRIOR APPLICATION NUMBER: PCT/US01/00666
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83.3%; Pred. No. 34;
                                                                                                 RESULT 7

US-10-116-788A-10

US-10-116-788A-10

Sequence 10, Application US/10116788A

Publication No. US20030170840A1

GENERAL INFORMATION:

APPLICANT: McDenaid, Thomas L.

APPLICANT: Meber, Annika

TITLE OF INVENTION: Genomic Mammary Amyloid A Sequence

FILE REFERENCE: P046557US1

CURRENT FILING DATE: 2002-06-10

FRIOR APPLICATION NUMBER: 09/425,679

PRIOR FILING DATE: 2000-06-10

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.1

SEQ ID NO 10
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APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47039, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-01-30
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Equus caballus
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100 HFRPHG 105
                                       ||:|||
HFRPHG 12
HFKPHG 7
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Guo, Xiaojia

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APPLICANT:
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                                                                                                                                                                                                                                                                                                     ery Match 63.6%; Score 35; DB 9; Length 244; st Local Similarity 71.4%; Pred. No. 1.7e+02; tches 5; Conservative 1; Mismatches 1; Indels
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: BLITTA.011A
CURRENT APPLICATION NUMBER: US/99/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PRILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-29
PRIOR PLING DATE: 2000-05-29
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2001-12-21
PRICH PRING DATE: 2001-12-21
PRICH PRING DATE: 2001-12-21
                                   MBER OF SEQ ID NOS: 14110
)FTWARE: FastSEQ for Windows Version 4.0
) ID NO 10094
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09-815-242-13891
equence 13891, Application US/09815242
atent No. US20020061569A1
ENERAL INFORMATION:
IOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Salmonella typhi
                                                                                                                                                                            TYPE: PRT
ORGANISM: Escherichia coli
9-815-242-10094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 RHVKPHG 107
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US-09-815-242-13891
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; Sequence 89, Application US/10120801 ; Publication No. US20030203843A1 ; GENERAL INFORMATION: ; APPLICANT: Pena, Carol

RESULT 11 US-10-120-801-89

101 RHVKPHG 107

1 KHFKPHG 7

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Gaps
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                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-340
CURRENT APPLICATION NUMBER: US/10/120,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: RENARD, STEPHANE
APPLICANT: RESNARD, STEPHANE
APPLICANT: GRAHAM, DAVID
APPLICANT: GRAHAM, DAVID
TITLE OF INVENTION: SODIUM CHANNEL RECEPTOR
FILE REFRENCE: 0.7586.0010
CURRENT APPLICATION NUMBER: 08/49/983,204
CURRENT FILING DATE: 2001-10-23
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/424,666
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1997-05-30
NUMBER: OF SEQ ID NOS: 19
SEQ ID NO 14
LENGTH: 512
                                                                                                                                                                                                                                                                                                                                                 CURRENT AFFILMS DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/285748
PRIOR APPLICATION NUMBER: 60/28608
PRIOR APPLICATION NUMBER: 60/28608
PRIOR APPLICATION NUMBER: 60/28608
PRIOR PILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/28632
PRIOR PILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/288334
PRIOR APPLICATION NUMBER: 60/291241
PRIOR APPLICATION NUMBER: 60/291241
PRIOR APPLICATION NUMBER: 60/291241
PRIOR APPLICATION NUMBER: 60/29284
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/285609
PRIOR APPLICATION NUMBER: 60/285609
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 155
SOOTWARRE: PRICATION NUMBER: 60/285609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/09983204; Patent No. US20020173000A1; GENERAL INFORMATION:
Shimkets, Richard
Padigaru, Muralidhara
                                                                                          Mehraban, Fuad
Topper, James N.
Malyankar, Uriel
Wasserman, Scott
                                                                                                                                                                                                                 Glennda
                                               Kekuda, Ramesh
Spytek, Kimberly
                                                                                                                                                                                       Edinger, Shlomit
                                                                                                                                                                                                                                 Gunther, Erik
Komuves, Laszlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 62.54
Matches 5; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                 Smithson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-983-204-14
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                                                                                                                                                                                                                                    APPLICANT:
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APPLICANT:
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144 KHYKPKQFS 152
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GENERAL INFORMATION:

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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Sequela, Philippe

TITLE OF INVENTION: A NOVEL HETERCOMULTIMERIC ION CHANNEL RECEPTOR AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: UNMERR: US/10/258,073

CURRENT FILING DATE: 2001-04-20

PRIOR RILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PATCHILIN VET: 2.1

SEQ ID NO 6

LENGTH: 512
                                                                                                                                                                                                                                                                                         RESULT 13
US-10-258-073-2
$ Gaquence 2, Application US/10258073
$ Fublication No. US20030219858A1
$ Fublication No. US20030219858A1
$ GENERAL INFORMATION:
$ APPLICANT: McGill University
$ APPLICANT: Babinski, Kazimierz
APPLICANT: 2001-04-08
$ CURRENT APPLICATION NUMBER: US/10/258,073
$ CURRENT APPLICATION NUMBER: PCT/CA01/00561
$ PRIOR PILING DATE: 2000-04-20
$ NUMBER OF SEQ ID NOS: 28
$ SOFTWARE: PatentIn Ver. 2.1
$ SEQ ID NO 2
$ LENGTH: 512
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                                                                     63.6%; Score 35; DB 10; Length 512; 66.7%; Pred. No. 3.7e+02; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.6%; Score 35; DB 12; Length 512; 66.7%; Pred. No. 3.7e+02; tive 1; Mismatches 2; Indels
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                                                                        Query Match 63.6
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 6; Conservative
; OTHER INFORMATION: MDEG
US-09-983-204-14
                                                                                                                                                                                                           ||:|| ||
144 KHYKPKQFS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 KHYKPKQFS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: HUMAN ASIC2A
US-10-258-073-2
                                                                                                                                                                            1 KHFKPHGFS 9
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; ORGANISM: RAT ASIC2A
US-10-258-073-6
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US-10-258-073-6
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RESULT 15
US-10-032-585-7813
is Sequence 7813, Application US/10032585
is Publication No. US2030180953A1
is GENERAL INFORMATION:
is APPLICANT: Terry, Roemer D.
is APPLICANT: Bo, Jiang
is APPLICANT: Bo, Jiang
is APPLICANT: Carles, Boone
is APPLICANT: Howard, Bussey
is TITLE OF INVERTIONS Gene Discuption Methodologies for Drug Target Discovery
if TITLE OF INVERTIONS DATE: US/10/032,585
is CURRENT APPLICANT: 2000-12-20
is CURRENT APPLICANT: A000-12-20
is SOFTWARE: PatentIn version 3.1
is SEQ ID NO 7813
is CRGANISM: Candida albicans
is SOFTWARE: PAT
is ORGANISM: Candida albicans
is COMERY Match
is Good of Mismatches Company of Company Company
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq-geneseqp-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1989.DAT:*
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| SIDSI/gcgdata/geneseqg-embl/AA1999.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqg-embl/AA1999.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqg-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqg-embl/AA2003.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqg-embl/AA2003.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqg-embl/AA2003.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-870-089B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description		Human cancer antiq	Novel human diagno	۳.		Human prostate can	Human cancer antic	Novel human diagno	Novel human diagno	Mouse ischaemic co
SUMMARIES			ID		ABG17297	AAG00153	ABG17298	AAB56718	AAU74680	ABG17300	ABG17299	ABB57035
•			DB DB	23	22	21	22	21	23	22	22	23
		•	Length	9	93	66	121	286	351	366	410	346
	οķο	Query	re Match Length DB I	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	89.1
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lori GHPO human dia moyl-phosp in encoded	e colos s serum thylhyd onorrho	Lung cancer-assoct Human novel polype Human liver peptid Human bone marrow Peptide #6786 enco	s the character of the	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Novel human diagno Arabidopsis thalia
AAW986 ABG243 AAR556 AAW564 ABB608	AAE0106 AAE0106 AAR2007 ABP7777 ABB6837	ABU5665 ABG9993 ABG5419 AAM7250 AAM3274 ABG4232		AAG2471 AAG2550 AAU3829 AAU3829 AAG25509 AAG25509	
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## ALIGNMENTS

RESULT 1 AAU74686

Human, cancer antigen, ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer. Human cancer antigen ATF4/CREB-2 natural immunogenic ligand. AAU74686 standard; Peptide; 9 AA. 09-APR-2002 (first entry) AAU74686; 

WO200192306-AZ.

Homo sapiens.

06-DEC-2001.

30-MAY-2001; 2001WO-US17454.

31-MAY-2000; 2000US-209388P. 20-DEC-2000; 2000US-257007P.

5

(GENZ ) GENZYME CORP.

Nicolette CA;

WPI; 2002-097764/13.

New therapeutic compounds comprising immunogenic ligands, useful for

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N-PSDB; AAS81484.
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                                                                      biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                             The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigon ATF4/CREB-2 (not defined) and the polynucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunoherapy comprising deministering to a subject the antibody, an immune effector cell that be been raised in vitro or in vivo in the presence and at the expense of an entitied presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune effector cell. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for generating anticularly covarian cancer. The compounds are useful for generating anticularly covarian cancer. The compounds are also useful for generating anticularly covarian cancer. The compounds are also useful for generating anticularly continuous are turber useful for immunotherapy when administered to a subject. The peptides, polypeptides and polynucleotides are useful in glannostic methods, for the defection and purification of antibodies,
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                                                                                                                                                                                                                                                                                                                        or as immunogens for the detection and purification of antibodies, sequence represents a human cancer antigen ATF4/CRBB-2 based immunogenic ligand of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 23; Length 9
100.0%; Pred. No. 9.3e+05;
tive 0; Mismatches 0; Indels
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                                         Claim 6; Page 56; 68pp; English
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23-AUG-2000; 2000US-0649167.
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Best Local Similarity
Matches 9; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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ABG17297
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The invention is sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (II) is useful in gene therapy techniques (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical charpothers involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Once the sequence data for this patent did not appear in the printed sequence in the invention.
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 22;
100.0%; Pred. No. 0.0099;
tive 0; Mismatches 0;
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                                                                                                                                                                                                         Claim 20; SEQ ID No 47656; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 KHFKPHGFS 46
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hes 9; Conserv
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                                                                                     The present sequence is a polypeptide encoded by one of a large number of 5. ESTs derived from mRNAs encoding secreted proteins. The 5. ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3. untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5. ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5. UTR is rarely included. 5. ESTs are derived from mRNAs with intact 5. ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5. ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                   diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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 correspond to 5'ESTs and
                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 55; DB 21; Length 99; 100.0%; Pred. No. 0.011; ive 0; Mismatches 0; Indels
                                                        Claim 13; SEQ ID 4234; 71pp + CD-ROM; English
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genomic DNAs that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #17289
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23-AUG-2000; 2000US-0649167.
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 cDNAs and
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                      99 AA;
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                                                                                                                                                                                                                                                                                                                                                        Sequence
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ABG17298
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for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAFIS566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal,
                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate cancer antigen protein sequence SEQ ID NO:1296.
                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 55; DB 22; Length 121; 100.0%; Pred. No. 0.013; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 1716-1718; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB56718 standard; Protein; 286 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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              and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAP16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
  nephrotropic, antiinfective, gynaecological and antibacterial activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cancer antigen; ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cancer antigen ATF4/CREB-2.
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20-DEC-2000; 2000US-257007P.
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                                                                                                                                                                                                                                                                                                                                                                         53 KHFKPHGFS 61
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N-PSDB; AAS20119.
                                                                                                                                                                                                                286 AA;
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                                                                                                                                                                           invention.
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especially useful in gene therapy or as components of anti-cancer vaccines. The compounds are useful for treating cancer, particularly ovarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These antibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polymucleotides are useful in diagnostic methods, for the detection and purification of antibodies, or as immunogens for the production of antibodies. The present sequence represents human cancer antigen ATF4/GREB-2 upon which the immunogenic ligands of the invention are based.
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #17291.
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                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      42 KHFKPHGFS
                                                                                                                                                                                                                    351 AA;
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ABG17300
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and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

410 AA;

Sequence

8888888

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30317 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                            100.0%; Score 55; DB 22; Length 366; 100.0%; Pred. No. 0.045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #17290.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG17299 standard; Protein; 410 AA.
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                                                                                                                                                                                                                                                                                                         1 KHFKPHGFS
                                                                                                                                                                                      366 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
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                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse ischaemic condition related protein sequence SEQ ID NO:43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
100.0%; Score 55; DB 22; Length 410; 100.0%; Pred. No. 0.051;
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                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                             ABB57035 standard; Protein; 346 AA
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                               Local Similarity 100.
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                                                                                                                      1 KHFKPHGFS
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Query Match
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DB 23; Length 346;

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Novel human diagnostic protein #24294.
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06-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including astroduced, chronic, and atrophic gastritis, and expette uloca diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.
                                                                                                                                                      GHPO protein, Helicobacter infection, gastroduodenal disease, gastritis, peptic ulcer disease.
          Gaps
                                                                                                                                                                                                                                                                                                                                                             New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 19; Length 348; Pred. No. 7.2; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                    Tomb J;
         Indels
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H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                   Oomen RP,
                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
(INWR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
Pred. No. 0.55;
          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 1444-1446; 2054pp; English.
                                                                                                                                                                                                                                                                                                                   Al-Garawi A, Kleanthous H, Miller C,
                                                                                      AAW98693 standard; Protein; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG24303 standard; Protein; 643 AA.
                                                                                                                                                                                                                                                       97US-0902615.
97US-0833457.
97US-0881227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.2%;
88.98;
                                                                                                                                                                                                                                      98WO-US06371.
                                                                                                                                        H. pylori GHPO 632 protein
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 87.5
                                      39 KHLKPHGFS 47
                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 HFKPHDFS 23
                                                                                                                                                                                   Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                   WPI; 1998-542293/46.
N-PSDB; AAX14412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 HFKPHGFS 9
                          1 KHFKPHGFS
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 AA;
                                                                                                                                                                                                    WO9843478-A1
                                                                                                                                                                                                                                                       29-JUL-1997;
01-APR-1997;
                                                                                                                                                                                                                                      01-APR-1998;
                                                                                                                                                                                                                                                                         4-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2002
                                                                                                                       31-MAR-1999
                                                                                                                                                                                                                      08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG24303;
                                                                                                       AAW98693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                     RESULT 10
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical insigning of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in changing it for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
Human, chromosome mapping; gene mapping; gene therapy, forensic; food supplement, medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 54662; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR55694 standard; Protein; 2391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
(first entry)
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les 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 HFKPHGQS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 HFKPHGFS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      643 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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us-09-870-089b-13.rag

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The present sequence is encoded by a testis 5' RACE clone type 1, created to characterise the 5' end of the human cancer cachectic factor (CCF) open reading frame. The coding region of CCF has extensive homology to a 20 amino acid sequence obtained from the peptide core of a mouse tumour derived proteoglycan with cachectic effects. CCF, a 24 kD protein factor, induces weight loss, and can be used with a substance capable of reducing appetite or inducing satiety. CCF can alternatively be campaintered with a substance capable of increasing the ratio of lean to fat body mass. CCF is useful for treating conditions or disorders arising from obesity or for inducing weight loss. CCF is used to prevent or treat non-insulin dependent diabetes (NIDDM) or Syndrome X. Anti-CCF antibodies can be used for direct application to cancer patients in order to reduce weight loss and tumour growth. The antibodies can used to diagnose cancer by detecting the presence of p24CCF in urine or serum of potential cancer patients. Antisense CCF gene constructs are useful for the prevention of unwanted endogenous synthesis or activity of CCF, e.g. in potential cancer patients, thus preventing weight loss (tissue degeneration). Labelled CCF or preventing of CCF24 kD CCF core peptide agonists.
                                                                        Human, cancer cachectic factor, p24K-inc, weight loss, treatment, mouse tumour derived proteoglycan, cachectic effect, prevention, non-insulin dependent diabetes, NIDDM, syndrome X, diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding a cancer cachectic factor - used to prevent or treat non-insulin dependent diabetes or Syndrome {\bf X}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 19; Length 119;
Pred. No. 8;
0; Mismatches 2; Indels
                                     Protein encoded by testis 5' RACE clone type 1.
                                                                                                                                                                                                                                                                                                                                                                                 Rasmussen PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB60839 standard; Protein; 1369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 36; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Clausen J, Din N, Farrah TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.7%;
77.8%;
                                                                                                                                                                                                                                                                   97WO-DK00377.
                                                                                                                                                                                                                                                                                                         96DK-0000968
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 KHFKPHSRS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KHFKPHGFS 9
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-207329/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV23110
                                                                                                                                                                                                                                                                                                     09-SEP-1996;
                                                                                                                                                                                        WO9811136-A1
                                                                                                                                                                                                                                                                   09-SEP-1997;
 05-AUG-1998
                                                                                                                                                                                                                              19-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB60839;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         쉱
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The cDNA sequence encoding the carbamoyl-phosphate-transferase II (CPSII) of Plasmodium falciparum was determined. The cDNA encodes a protein that includes 2 insert sequences not found in other CPSII proteins. The first separates the putative structural subdomain and the glutaminase subdomain of the glutamine-amidotransferase subunit cPSII, while the second separates 2 ATP binding subdomains of the CPSII subunit, CPSa and CPSD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding carbamoyl phosphate synthetase II - isolated from Plasmodium falciparum, used to develop prods. for the treatment of malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                /note= "carbamoyl-phosphate-synthase domain"
691..1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2391;
                                                                                                                                                                   'note= "glutamine-amidotransferase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                   Carbamoyl-phosphate-synthetase II; CPSII; psCPSII gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "ATP binding subdomain CPSb"
                                                                                                                                                                                                                                                                                                                                                  /note= "ATP binding subdomain CPSa
1255..1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 15;
Pred. No. 1.4e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                 "glutaminase subdomain"
                                                                                                                                                                                                        "structural subdomain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                             /note= "insert sequence"
1858..2391
                                                                                                                                                                                                                                                "insert sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 6-16; 31pp; English.
                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW56455 standard; Protein; 119 AA.
Carbamoyl-phosphate-synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92AU-0006206.
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|168 KYFKKHGFS 1176
                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                   /note=
                                                                                        Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ62924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9412643-A1
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                                                           malaria
                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                   Domain
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                                                                                                                                                                                                                                                                 Domain
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Vissing H;

; 0

Gaps

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Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster polypeptide SEQ ID NO 9309.

AAW56455

RESULT 13 AAW56455

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McDonald TL,
                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                              detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Horse, colostrum; serum amyloid A; SAA; antibacterial; antidiarrhoeic; apolipoprotein; inflammatory response; mucin 3; MUC3; therapy; Escherichia coli infection; traveller's diarrhoea; infant diarrhoea; necrotising enterocolitis; NBC; urinary tract infection; dysentery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 9309; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horse colostrum-associated serum amyloid A (SAA) peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.1%; Score 38; DB 22; L
100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0;
                                                                                                                                                                      Myers EW;
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                                                                                                                                                                      Li PWD,
                                                                                                              23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                        23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-OCT-2000; 2000WO-US29065.
                                                                                                                                                                                                                             New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
--haq 6, Conserva
                                                                                                                                                                      Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infectious diarrhoea
                                                                                                                                                                                            WPI; 2001-656860/75
N-PSDB; ABL04942.
                                                                                                                                                                                                                                                                                                                                                                               (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              571 FKPHGF 576
                                                                                                                                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                     1369 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 FKPHGF
 pharmaceutical.
                                            WO200171042-A2
                                                                                                                                                                                                                                                   interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Equus caballus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-2001
                                                                   27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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The patent discloses novel colostrum-associated Serum Amyloid A (SAA) from mammals. SAAs are small apolipoproteins that accumulate and associate rapidly with high-density lipoprotein 3 (HDL3) during the acute phase of inflammatory response. They are characterised by the TFLK motif in the N-terminal region which has the ability to stimulate mucin 3 (MCG3) production. Colostrum associated SAAs are used to prevent or treat infectious diseases associated with enteric pathogens (particularly Bscherichia coli) such as traveller's diarrhoea, infant diarrhoea, necrotising enterocolitis (NEC), urinary tract infections, and infectious diarrhoea in herd animals. They are used to prevent dysentery and other infectious diseases particularly for the military.
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                                                                                                                                                                                                                                                                                                                                     New colostrum-associated serum amyloid A protein induces mucin production in epithelial cells and is useful to prevent and treat
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Pred. No. 3.4;
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                                                                                                                                                                                                  Mack DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 20; 81pp; English
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83.3%;
22-OCT-1999; 99US-0425679.
14-JUL-2000; 2000US-0218482.
17-JUL-2000; 2000US-0218611.
                                                                                                                                                                                                                                                                                                                                                                                                       enteric pathogen infection
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                                                                                                                                   (UYNE-) UNIV NEBRASKA
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Matches 5; Conser
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G protein-co taste recept novel G-prot

G-protein co acid sequenc human diagno immune/haema

Minimum DB s Maximum DB s

Database

Result No.

Searched:

polypeptide polypeptide

taste cell s

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normal

OM protein

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Run

Sequence:

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Staphylococcus epi
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Human novel G-prot
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ABP40155
ABB11608
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ABB77319
ABP70449
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AAU28065
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ABP81751
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ABB96319
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AAW58530
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AAO03783
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 31-MAY-2000; 2000US-209388P.
20-DEC-2000; 2000US-257007P.
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WO200192306-A2.
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Synthetic.
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 Human muskelin. H
Human EXMAD-4 SEQ
Arabidopsis thalia
Arabidopsis thalia
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Human protein sequ
Human protein SEQ
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(without alignments)
43.289 Million cell updates/sec
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| SiDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SiDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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| SiDSI/gcgdata/geneseq-embl/AA2002.DAT:*
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                                                                                                                                                                                                                  1107863
       GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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                                                                       2003, 14:06:05
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Maximum Match 100%
Listing first 45 summaries
                                                    - protein search, using sw model
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AAB53260
AAB93552
AAM79281
AAB77226
AAB27226
AAG24107
AAG06848
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Gapop 10.0 , Gapext 0.5
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer artigen ATF4(FREB-2 (fout defined) and the polymucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising the compound, a method of immunotherapy comprising administering to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of antigen presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response to the synthetic and naturally occurring compounds. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for treating cancer, particularly vaccines. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These compounds are also useful for generating antibodies cut the peptides, for the detection and purification of antibodies, or as immunogen for the production of antibodies. The present
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New therapeutic compounds comprising immunogenic ligands, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   but have not been cross-referenced or CDS features put in due to the
                                  modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
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                                                                                                                                            Claim 5; Page 56; 68pp; English.
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigan ATP4/CRBB-2 (not defined) and the polymucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, an ethod of immunotherapy comprising delivering the compound, an intended of immunotherapy comprising to a subject the antibody, an immuno effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antigen presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response effector cell. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are especially useful in gene therapy or as components of anti-cancer vaccines. The compounds are useful for treating cancer, particularly contexts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ovarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These autibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polynucleotides are useful in diagnostic methods, for the detection and purification of antibodies, or as immunogens for the production of antibodies. The present sequence represents a human cancer antigen ATF4/CREB-2 based immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respectively but have not been cross-referenced or CDS features put in due to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective, vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; infectious disease; cardiovascular disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                    New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
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Pred. No. 9.3e+05;
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                                                                                                                                                                                   Claim 2; Page 55; 68pp; English
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77.8%;
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                                           WPI; 2002-097764/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200055351-A1
Nicolette CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB53260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostafic, cardioactive, muscular; human colon cancer antigens can have cytostafic, cardioactive, muscular; culnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent disorders, reproductive disorders, immune system disorders, muscular disorders, reproductive disorders, immune gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAC98707 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                   Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                        80.0%; Score 40; DB 21; Length 148; 100.0%; Pred. No. 7; or Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein sequence SEQ ID NO:12932.
                                                                                                                                                             Claim 11; Page 1356; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB93552 standard; Protein; 528 AA.
                                                                                                                               antigens, useful for the treatmer
disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                            (HUMA-) HUMAN GENOME SCI INC
08-MAR-2000; 2000WO-US05883.
                     99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity luv...
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HELI-) HELIX RES INST
                                                                 Rosen CA, Ruben SM;
                                                                                     WPI; 2000-587534/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHKVHYL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                                                      148 AA;
                                                                                                N-PSDB; AAC98017.
                                                                                                                                                                                                                                                                                                                                                                                                                                     LHKVHYL
                     12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                  invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB93552;
                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nuclectide comprises at least 15 nuclectides; or (b) a combination of alignounclectide comprises a least 15 nuclectides; or (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 3'-end sequence complementary to a polynuclectide comprises a 3'-end sequence complementary to a polynuclectide comprises a 3'-end sequence complementary to a complementary strand of a sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the full-length cDNAs. The primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH13618 and AAH13631 to AAH13631 to AAH13632 to AAH13632 to PAH13632 and AAH36391 represent human amino acid sequences; and AAH13632 to AAH13632 cepresent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
           Saito K, Yamamoto J;
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID 12932; 2537pp + CD ROM; English.
       hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 26; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM79281 standard; Protein; 735 AA.
Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein SEQ ID NO 1943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0620325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-FEB-2001; 2001WO-US04098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  387 LHKVHYL 393
                                                                                                                       WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LHKVHYL 8
                                                                                                                                                                                                                                                                                                                  Full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       528 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
   Ota T, Is
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM79281;
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99US-0133643.
99US-0150409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .0-MAY-2000; 2000WO-US12811
                                                                                                                                                                                                                                                                                                                                               Human EXMAD-4 SEQ ID NO: 4.
                                                                                                                                                                                                                                                                                                                          27-MAR-2001 (first entry)
                                                                                                                                                                             Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillman JL,
                                                                                                                                                                                                                               594 LHKVHYL 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-007395/01.
                                                                                                                                                                                                           2 LHKVHYL 8
                                                                                                                                              735 AA;
 N-PSDB; AAF81521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC66893.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200068380-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bandman O,
Azimzai Y;
                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                     AAB27226;
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                             The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, nematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                      Ma Y;
                                                                                                                                                                                                                                                                                            treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           muskelin; AIDS; retrograde neuropathy; topical anaemic damage; development deficiency; osteopathy.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                      Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                  Drmanac RT, Asundi V, Zhou P, Xu C, Ca
Wang J, Zhang J, Ren P, Chen R, Wang
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 40; DB 22; Length 735; 100.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHAN-) SHANGHAI BIORIGIN GENE DEV CO LTD.
                                                                                                                                                                           Claim 20; Page 4349-4350; 6221pp; English
                                                                                                                                                        useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB73094 standard; Protein; 735 AA.
01-SEP-2000, 2000US-0654936.
15-SEP-2000, 2000US-0653561.
20-OCT-2000, 2000US-0693325.
30-NOV-2000, 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-2000; 2000WO-CN00269.
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry
                                                                                                                                                                                                                                                                                                                                                                                                                                      594 LHKVHYL 600
                                                                                                             WPI; 2001-476283/51
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                                                                    Liu C, D
Wang D,
Yang Y, W
                                                                                                                                                                                                                                                                                                                                                                                                                    2 LHKVHYL 8
                                                                                                                                                                                                                                                                                                                                                        735 AA;
                                                 (HYSE-) HYSEQ INC.
                                                                                                                        N-PSDB; AAK52414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human muskelin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-2001
                                                                      Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73094;
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                          Kue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a novel human muskelin. The sequences are useful in the treatment of acquired immunodeficiency syndrome (AIDS), retrograde neuropathy, spinal development deficiency, topical anaemic damage, osteopathy, malignant tumours and chronic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences for 25 novel extracellular matrix and adhesion-associated proteins (EXMADS). These are designated EXMAD-1, EXMAD-2, EXMAD-10, EXMAD-1, EXMAD-1, EXMAD-1, EXMAD-1, EXMAD-13, EXMAD-13, EXMAD-13, EXMAD-14, EXMAD-12, EXMAD-17, EXMAD-17, EXMAD-21, EXMAD-22, EXMAD-23, EXMAD-24, and EXMAD-25. They are useful in the prevention and treatment of cancers, cell proliferation,
                                      topical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular matrix and adhesion-associated protein; EXMAD; cancer; inflammation; reproductive disorder; cardiovascular disorder; immune disorder; musculoskeletal disorder; developmental disorder; gastrointestinal disorder; cell proliferation disorder.
New muskelin polypeptide, for treating acquired immunodeficiency syndrome, retrograde neuropathy, spinal development deficiency, to anemic damage, osteopathy, malignant tumor and chronic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polynucleotide encoding extracellular matrix or adhesion-associated protein (EXMAD) useful for diagnosing, treatibreenting disorders associated with expression of EXMAD such as proliferative, immune and genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%; Score 40; DB 22; Length 735; 100.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ή,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 90-92; 129pp; English.
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                                                                                                                                                      Claim 1; Page 21-23; 27pp; Chinese
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05-MAR-1999,
23-MAR-1999,
25-MAR-1999,
11-APR-1999,
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119-APR-1999,
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23-APR-1999,
30-APR-1999,
06-MAY-1999,
06-MAY-1999,
06-MAY-1999,
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11-MAY-1999,
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-MAY-1999;
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                                       AAG24453;
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-MAY-1
-MAY-1
  RESULT 10
            AAG24453
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
              Arabidopsis thaliana protein fragment SEQ ID NO: 3773.
                                                                                                                                                                       990S - 0.121825
990S - 0.1218180
990S - 0.123180
990S - 0.125788
990S - 0.126785
990S - 0.126785
990S - 0.1208134
990S - 0.1208145
990S - 0.130819
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99US-0139119.
99US-0139119.
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990S-0139461.
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                                                                               Arabidopsis thaliana
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06-APR-1999;
08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
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06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
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04-MAY-1999;
05-MAY-1999;
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01-JUN-1999;
03-JUN-1999;
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Pred. No. 89;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG06847 standard; Protein; 378 AA.
99US-0149929
99US-0149920
99US-0149902
99US-015066
99US-0151066
99US-0151066
99US-0151080
99US-0151080
99US-0151303
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99US-015139
99US-0155139
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99US-0155139
99US-0151330
99US-015933
99US-016933
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ilarity 75.0%;
Conservative
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FLHKIHRL 59
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                 24-SEP-1999
28-SEP-1999
04-OCT-1999
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13-OCT-1999
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 20-AUG-1999;
23-AUG-1999;
25-AUG-1999;
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27-AUG-1999;
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31-AUG-1999;
31-AUG-1999;
10-SEP-1999;
11-SEP-1999;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB48228 standard; Protein; 454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.0%;
71.4%;
990S-0151080
990S-0151303
990S-0151303
990S-0151303
990S-0151306
990S-0153758
990S-0154019
990S-0154019
990S-0154079
990S-015559
990S-0155659
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990S-015629
990S-015929
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99US-0161405
99US-0161406
99US-0161350
99US-0161360
99US-0161361
99US-0161923
99US-0161993
99US-01611993
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Best Local Similarity 71.4
Matches 5; Conservative
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89 HKIHYVV 95
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27-Aug-1999)
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N-PSDB; ABL07831
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                                 27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for bodynessis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome card proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. Monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                  Dehoux P;
Cossart P;
                                                                                                                                                                                                                                                                                                                             Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                                                                    Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart F Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Chakrbit A, Durant L, Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Rose M, Voss H, Hauf J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 17976.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; SEQ ID No 933; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB63728 standard; Protein; 979 AA.
                                                                          11-APR-2001; 2001WO-FR01118.
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Conservative
                                                                                                      11-APR-2000; 2000FR-0004629
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239 YLHKLHY 245
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Best Local Similarity
Matches 5; Conserv
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              WO200177335-A2
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                                             18-OCT-2001
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X S X M M X E X H X Y X H
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                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention signiscines genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB27137-ABB72072).
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Pred. No. 2.8e+02;
2; Mismatches 0;
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                                                                                                                                     PWD,
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23-MAR-2001; 2001WO-US09231
                                      23-MAR-2000; 2000US-191637P.
                                                      11-JUL-2000; 2000US-0614150
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity 71.*.
Si Conservative
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                                                                                                                                   Venter JC, Adams M,
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                                                                                             (PEKE ) PE CORP NY
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0
                                                                                                                                   capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABLi6176-ABLi6176) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer antigen; ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATF4/CREB-2 (not defined) and the polynucleotides encoding them.
                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                            Disclosure; SEQ ID NO 24660; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                     72.0%; Score 36; DB 22; Length 1084; 55.6%; Pred. No. 3.1e+02; tive 3; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cancer antigen ATF4/CREB-2 based immunogenic ligand #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU74683 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 55; 68pp; English
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20-DEC-2000; 2000US-257007P.
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WPI; 2001-656860/75.
N-PSDB; ABL10059.
                                                                                                                                                                                                                                                                                            Sequence 1084 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicolette CA;
                                                                    interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU74683;
                                                                                                                                                                                                                                                                                                                        Query Match
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compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising delivering the compound, a method of immunotherapy comprising the compound, a method of immunotherapy comprising deflictor call that has been raised in viero or in vivo in the presence and at the expense of an antigen presenting cell that presents the immunogenic compound in the context of an MFC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response of the synthetic and naturally occurring compounds in menne capecially useful in gene therapy or as components of anti-cancer vaccines. The compounds are useful for treating cancer, particularly covarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These current useful for immunotherapy when administered to a cubject. The peptides, polypeptides and polynucleocides are useful in diagnostic methods, for the detection and purification of antibodies.

Sequence represents a human cancer antigen ATF4/CREB-2 based immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
Also included are an antibody that specifically recognises and binds the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ligand of the invention.

Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respectively but have not been cross-referenced or CDS features put in due to the degeneracy of the DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December 16, 2003, 14:14:30
Job time : 34 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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FLHKWHWVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Sequence 36, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 6; Conservative
MOLECULE TYPE: protein US-08-378-939-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 HKVHYL 39
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 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 710, Ap
Sequence 731, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 2106, Appl
Sequence 63, Appl
Sequence 13, Appl
Sequence 29014, Appl
Sequence 29014, Appl
Sequence 29014, Appl
Sequence 29014, Appl
Sequence 5381, Appl
                                                                    December 16, 2003, 14:11:00 ; Search time 12.3333 Seconds (without alignments) 30.875 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                          1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-100-851-1

US-09-265-294-1

US-09-215-694-1

US-09-328-352-7101

US-08-328-352-7331

US-08-937-155-19

US-08-937-155-19

US-09-937-155-19

US-09-937-15-19

US-09-37-15-19

US-09-126-420A-23

US-09-126-420A-23

US-09-126-420A-23

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

US-08-477-346-63

US-07-752-101A-68

US-07-752-101A-68

US-07-752-101A-68

US-09-732-210-1619

US-09-732-210-1619

US-09-732-210-1619

US-09-732-210-1619

US-09-732-210-1619

US-09-732-210-1619

US-09-732-210-1619

US-09-732-210-1619

US-09-732-210-1619

US-09-732-310-318-35-5381

US-07-752-101A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-378-939-36
US-09-134-001C-5000
                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                            328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
                                                                                                                                                                                                                                       length: 0
length: 2000000000
                                                                                                                  US-09-870-089B-11
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Match Length DB
                                                                                                                                       1 FLHKVHYLV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                      Minimum DB seq
Maximum DB seq
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                                                                                                                                                                                             Searched:
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                                                                         Run on:
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No.
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0;
                                                                  52, Appl
2, Appli
3, Appli
3, Appli
3, Appli
33130, A
4407, Ap
111, App
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                    Sequence
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US-07-752-101A-38
US-07-752-101A-39
US-07-752-101A-41
US-07-752-101A-51
US-07-752-101A-52
US-07-761-101A-52
US-07-841-651-2
US-07-841-651-3
US-09-328-352-7436
PCT-US44-00138-3
US-09-328-352-4407
US-08-378-352-4407
US-08-481-905-111
US-08-370-476-111
US-08-370-476-111
US-08-370-476-111
US-08-370-476-111
US-08-370-455-7
US-09-3134-651-7
US-09-3134-651-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THRITEENTH ST. N.W.
CITY MASHINGTON
STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.0%; Score 36; DB 2; 100.0%; Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECHONE: (202) 783-6040
TELECHONE: (202) 783-6041
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
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                                                                                                                                                                                    68.0%; Score 34; DB 1; Length 311; 71.4%; Pred. No. 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-09-100-851-1
Sequence 1, Application US/09100851
Patent No. 5911984
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi)
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILLING DATE:
FILLING DATE:
                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/872,784
APTING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION WUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0293 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/09265294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
THE COMPUTER: DISKETTE
THE COMPATIBLE
THE COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                      Best Local Similarity 71.4
Matches 5; Conservative
                    ; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT09
; CLONE: 2150905
US-08-872-784-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: BRAINOT09
CLONE: 2150905
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239 HKVHFMV 245
linear
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Matches 5; Conserv
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US-09-265-294-1
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                                                                                                                                                                                           Query Match
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                                                                                               Sequence 5000, Application US/09134001C

Redent No. 6380370
GRNEAL INFORMATION:
GRNEAL INFORMATION:
GRNEAL INFORMATION:
TITLE OF INVENTION: BULGETC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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Pred. No. 39;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi,
APPLICANT: Shah, Purvi,
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,784
FILING DATE: Filed Herewith
PKIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5000
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FILING DATE:
ATGAREY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0.
TELECOMMUNICATION INFORMATION:
TTLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-872-784-1; Sequence 1, Application US/08872784; Patent No. 5776753
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55.6%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||:::||
114 YLHKINFLV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FLHKVHYLV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                        JS-09-134-001C-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
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Length 1068;
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50.0%; Pred. No. 68;
1ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.0%; Score 33; DB 4; Length 157; 44.4%; Pred. No. 73; tive 4; Mismatches 1; Indels
68.0%; Score 34; DB 4; Length 106 ilarity 71.4%; PredC No. 31e+05. Conservative 8; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                   US-09-328-352-7101
; Sequence 7101, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 44.4 Matches 4; Conservative
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116 FMHEIHALI 124
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185 FLHRVHH 191
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71 IHKAHYIL 78
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Query Match
Best Local Similarity
Matches 5; Conserv
                                                                         1 FLHKVHY 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 157
TYPE: PRT
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Patent No. 6391581
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wisconsin Alumni Research Foundation
APPLICANT: Hutchinson, Charles R.
APPLICANT: Kennedy, Jonathan n.m.i
APPLICANT: Park, Checnseck n.m.i
ITILE OF INVENTION: METHOD OF PRODUCING ANTHYPERCHOLESTEROLEMIC AGENTS
FILE REFERENCE: 960296.95718
CURRENT APPLICATION NUMBER: 187/09/215,694B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PEROXISOMAL THIOESTERASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0293 US
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,851
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LENGTH: 1068
; TYPE: BRT
; ORGANISM: Aspergillus terreus
US-09-215-694-7
                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 amino acids
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Best Local Similarity 71...
hea 5; Conservative
                                                                                                                                                                                                                                     ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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SOFTWARE: Patentin Ve
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STRANDEDNESS: sin
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                                                                                                                                                               STREET: 3174 Por
CITY: Palo Alto
STATE: CA
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Patent No. 6210890
GENERAL INFORMATION:
                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                       COUNTRY:
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US-09-215-694-7
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Sequence 7331, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION UNDEER: US/09/328,352
CURRENT APPLICATION UNDEER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7101
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; Patent No. 5744341
; GENERAL INFORMATION:
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
; TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Gaps
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KELBER, STEVEN B.
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Sequence 19, Application US/08937155

Patent No. 6524811

GENERAL INFORMATION:

APPLICANT: CUNINGHAM JR., FRANCIS X.

APPLICANT: SUN, ZAIREN

TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND
TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.0%; Score 33; DB 1; Length 288; 50.0%; Pred. No. 1.3e+02; tive 4; Mismatches 0; Indels
                ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,125
FILING DATE: 29-MAR-1996
CLASSIFICATION:
NAME: KELBER, STEVEN B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747-063-27
TELEPHONE: 709-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/624,125
FILING DATE: 29-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECCURION: 703-413-220
TELEFAX: 703-413-220
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TVPB: amino acids
TVPB: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||:::||:
189 FLNRIHYM 196
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-624-125-19
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WES-09-126-420A-20
Sequence 20, Application US/09126420A
Sequence 20, Application Salvanion
APPLICANT: BATARD, YANNICK
APPLICANT: ROBINEAU, LUC
TITLE OF INVENTION: PURIFIED CYTOCHORME P450 CYP76B1 FROM HELIANTHUS
TITLE OF INVENTION: PURIFIED CYTOCHORME P450 CYP76B1 FROM HELIANTHUS
TITLE OF INVENTION: PURIFIED CYTOCHORME P450 CYP76B1 FROM HELIANTHUS
TITLE OF INVENTION: PURIFIED CYTOCHORME P450 CYP76B1 FROM HELIANTHUS
TITLE OF INVENTION: PURIFIED CYTOCHORME P450 CYP76B1 FROM HELIANTHUS
TITLE OF INVENTION: POLLUTANTS AND FOR ALTERING THE RESISTANCE OF PLANTS S
FILE REFERENCE: 03715.0032
CURRENT FILING DATE: 1998-07-30
PRIOR PILING DATE: 1997-07-31
SOFTWARE: PATENTING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET. 2.1
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APPLICANT: BOUNG-JUN, OH
APPLICANT: MOON, KYUNG KO
APPLICANT: MOON, KYUNG KO
APPLICANT: YOUNG, SCONKIM
TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
TITLE OF INVENTION: INCOMPATIBLE INTERACTION
FILE REFERENCE: 10324/P64443USO
CURRENT APPLICATION NUMBER: US/09/499,302A
CURRENT FILING DATE: 2000-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                       Length 288;
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                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 4; Length 288
Pred. No. 1.3e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.0%; Score 33; DB 4; Length 471 Best Local Similarity 71.4%; Pred. No. 2.1e+02; Matches 5; Conservative 2; Mismatches 0; Indels
                                  2747-063-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09499302A
Patent No. 6369212
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-2220
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          66.0%;
50.0%;
                                                                                                                                                                                           LENGTH: 288 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.v.
--- 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Persea americana
                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-937-155-19
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189 FLNRIHYM 196
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                                                                                                                                                                                                                                                       APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPENDENCE ADDRESS:
ADDRESSE: Delinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 63, Application US/08477346

Patent No. 6262023

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
ITILE OF INVENTION: WD-40 - Derived Peptides and Uses
ITILE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MELLUM IIE. FLOURY LESS
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
FILING DATE: 01-FEB-1994
CLASSIFCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0960
TELEPHONE: (415) 324-0960
TELEPHONE: (415) 324-0960
TELERAX: (415) 324-0960
SUNFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TUP1, Fig. 46
                                                                                                                                                            US-08-190-802A-63
Sequence 63, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 713 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 LHQDHYLV 286
                                                         259 LHQLHYL 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94306-0850
                               2 LHKVHYL
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US-08-477-346-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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STATE:
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Sequence 2105. Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR PRILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
TYPE: PRT
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.0%; Score 33; DB 4; Length 502; 71.4%; Pred. No. 2.2e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (199)
OTHER INFORMATION: variable or unknown amino acid
NAMB/KEY: MOD_RES
LOCATION: (126)
OTHER INFORMATION: variable or unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (240)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (247)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD RES
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                        LOCATION: (30)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD RES
LOCATION: (49)
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OTHER INFORMATION: variable or unknown amino acid
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NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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Matches 5; Conserv
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                                                                                                TYPE: PRT
ORGANISM: Persea sp
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LOCATION: (240)
                                                                                                                                                              NAME/KEY: MOD_RES
                                                                                                                                                                                                                                 NAME/KEY: MOD_RES
LOCATION: (22)
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                                                                                                                                                                                      LOCATION: (1)
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Query Match 66.0%; Score 33; DB 3; Length 713; Best Local Similarity 75.0%; Pred. No. 3.1e+02; Matches 6; Conservative 1; Mismatches 1; Indels
CITY: Washington
STATE: DC
CONTRY: USA
ZIP: 20006-1812
COMPUTER READBLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
ATTORNEY/ASMY INFORMATION: 514
PRIOR APPLICATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/COMMUNICATION INFORMATION:
TELEPRAM: (202) 887-1500
TELEPRAM: (202) 887-1500
TELEPRAM: TAI amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOUGHE: TUPI, Fig. 46
US-08-477-346-63
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Gaps o;

Search completed: December 16, 2003, 14:20:41 Job time : 13.3333 secs

qq

Run on:

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1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-1973-9-19
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probable CHP-rich
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: T47173
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Well, B.; Wiemann, S. submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24376
A;Reference number: Z24376
A;Reference number: March 2000
A;Reference number: A;Reference num
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A) Experimental Bource: adult melanoma (MeWo cell line); clone DKFZp7621156 C)Genetics:
A)Note: DKFZp7621156.1
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                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                        A34440
T29416
A35867
T31717
T34193
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F85024
T10575
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G85024
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C82714
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   0000000000000000
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Best Local Similarity 100.
Matches 6; Conservative
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 275 LHKVHYL 281
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                (without alignments)
83.760 Million cell updates/sec
                                                                                                                                2003, 14:10:15 ; Search time 10.3333 Seconds
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                   GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                        283308 seqs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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F30534
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AF1217
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T38986
T29415
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H91275
AG1052
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Gapop 10.0 , Gapext 0.5
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1 FLHKVHYLV 9
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Maximum DB seq length: 2000000000
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Match Length DB
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                                   Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
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                                                                                           OM protein
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Database

Result 8

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A;Residues: 1-113 CLA> C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-96/Domain: immunoglobulin homology <IMM>

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-113 <CLA

72.0%; Score 36; DB 2; Length 113; 100.0%; Pred. No. 6.9;

0; Mismatches

6; Conservative

34 HKVHYL 39

3 HKVHYL 8

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Best Local Similarity

Query Match Matches

Indels

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A;Accession: 03538
A;Status: preliminary: nucleic acid sequence not shown; not compared with conceptual transmostatus: preliminary: nucleic acid sequence not shown; not compared with conceptual transmosts. 22-104 cCL7>
A;Residues: 32-104 cCL7>
A;Residues: 32-104 cCL7>
A;Experimental source: 253.1265
A;Experimental source: 253.1265
Lain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology cIMM>
F;16-96/Domain: immunoglobulin homology cIMM>
F;23-94/Disulfide bonds: #status predicted
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C'Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: C85431
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprir. Nature 402, 769-777, 1999
                                                                             A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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A;Accession: C30538
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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A;Accession: C85431
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A;Molecule type: DNA
A;Residues: 1-378 <STO>
A;Residues: 1-378 <STO>
A;Cross-references: GB:NC_001268; NID:g7270601; PIDN:CAB80319.1; GSPDB:GN00140
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                                                                                                                                                                        A)Residues: 1-106 <CLA>
A)Experimental source: clone 252.5E10
A)Accession: D30534
A)Status: preliminary; not compared with conceptual translation
A)Molecule type: mRNA
A)Residues: 1-104 <CL2>
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A; Status: preliminary; not compared with conceptual translation A; Molecule type: mRNA
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A,Accession: G30534
A,Status: preliminary; not compared with conceptual translation
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A;Reference number: A30534; MUID:89035545; PMID:3141511
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Pred. No. 25;
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A;Experimental source: clone 252.5E11
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71.4%;
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A;Map position: 4
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C;Species: Mus musculus (house mouse)
C;Species: Norse musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 21-Jan-2000
C;Accession: F30534
S;Claflin, J.L.; Berry, J.
J mmuunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu A;Reference number: A30534; MUID:89035545; PMID:3141511
A;Accession: F30534
A;Accession: F
                                                                                                                                                                        Ig kappa chain V region (224.4B11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 21-Jan-2000
C;Accession: H30534
R;Claflin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu A;Reference number: A30534; MUID:89035545; PMID:3141511
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;16-96/Domain: immunoglobulin homology <IMM>

A; Residues: 1-113 <CLA>

Length 113;

0; Indels

72.0%; Score 36; DB 2; 100.0%; Pred. No. 6.9; iive 0; Mismatches

6; Conservative

34 HKVHYL 39

3 НКУНУГ 8

Query Match Best Local Similarity Matches 6; Conserv

Ig kappa chain V region (S107A) - mouse

RESULT 5 KVMS7A

A; Molecule type: mRNA A; Residues: 1-114 < KWA> A; Note: Les sequents as determined from the differentiated gene R; Clafilin, J.L.; Berry, J. J. Immunol. 141, 4012-4019, 1988

A; Accession: A01915

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A;Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15139.1; PID:g38612.
A;Experimental source: strain Madrid E
cytochrome C-type biogenesis protein comF (comF) RP703 - Rickettsia prowazekii CiSpecies: Rickettsia prowazekii CiSpecies: Rickettsia prowazekii CiDate: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C;Accession: C71630 R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998 A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
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A;Molecule type: DNA
A;Residues: 1-300 <MCD.
A;Residues: 1-300 <MCD.
A;Residues: BMBL;AL109832; PIDN:CAB52730.1; GSPDB:GN00066; SPDB:SPAC630.08c
A;Experimental source: strain 972h-; cosmid c630
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                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-670 <AND>
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C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Actesion: T18438
R;Lawson, D.; Bowman, S.; Barrell, B.
Submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Reference number: Z18935
A;Accession: T18438
A;Catus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1532 <LAW>
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Pred. No. 1.1e+02;
2; Mismatches 1; Indels
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Pred. No. 47;
1; Mismatches 1; Indels
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C;Superfamily: Saccharomyces cerevisiae ERG25 protein
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Best Local Similarity 66.7%;
Matches 6; Conservative 2
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Matches 6; Conservative
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A;Gene: ccmF; RP703
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A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 31;
2; Mismatches (
         Mismatches
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239 YLHKLHY 245
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239 YLHKLHY 245
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Best Local Similarity
Matches 5; Conserv
                                                                                              з нкинхги 9
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A;Molecule type: DNA
A;Residues: 1-454 <GLA>
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WXIHXM
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A;Gene: lmol142
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Best Local Similarity 62.5
Matches 5; Conservative
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970 FLHRLHHL 977
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C;Species: Ciona intestinalis
C;Species: Ciona intestinalis
C;Date: 22-2an-1999 #sequence_revision 22-Jan-1999 #text_change 23-Mar-2001
C;Accession: T00094
R;Ogasawara, M; Satoh, N.
Satoh, N.
Submitted to the EMBL Data Library, Pebruary 1998
A;Description: Isolation and characterization of endostyle-specific genes in the Ascidia
A;Reference number: Z14109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C'Species: Caenorhabditis elegans
C'Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
C'Accession: T29415
R;Wilson, R.; Favello, A.; Le, T.T.
submitted to the EMBLD Data Library, April 1997
A;Description: The sequence of C. elegans cosmid F21F8.
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Score 35, DB 2; Length 300;
Pred. No. 31;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F21F8.9 - Caenorhabditis elegans
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A;Status: prellminary: translated from GB/EMBL/DDBJ
A;Accelle type: DNA
A;Residues: 1-347 <WIL>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-650 <0GA>
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A;Introns: 67/3; 97/1; 123/2; 215/3; 258/3; 318/1
         70.0%;
71.4%;
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    Query Match
Best Local Similarity 71.4*
Matches 5; Conservative
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10 YLHSIHYI 17
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                            1 FLHKVHY 7
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Cispecies: Babesia bowls
Cispecies: Babesia bowls
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Cipate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
Cispeciesion: T3139
Cispeciesion: T31314, 1996
A;Title: Sequences upstream and downstream from the glutamine-dependent carbamoyl phosph A;Reference number: Z21005; MUID:96257278; PMID:8654985
A;Reference number: Z21005; MUID:96257278; PMID:8654985
A;Recession: T31339
A;Recession: T31339
A;Recession: T3134
A;Molecule type: DNA
A;Residues: 1-1645 < AAG-
A;Coss-references: EMBL:U18792; NID:9944893; PID:g619743; PIDN:AAC47302.1
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C;Superfamily: carbamoyl-phosphate synthase (ammonia); biotin carboxylase homology; carb
omology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG
C;Keywords: ligase
F;26-1623/Domain: carbamoyl-phosphate synthase (ammonia) homology <CPA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) III - Babesia bovis
Science 293, 2093-2098, 2001
A,Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A,Reference number: A97700; MUID:21442074; PMID:11557893
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                                                                                                    A; Accession: H97834
A; Status: preliminary
A; Odecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1.662 < KUR>
A; Cross-references: GB: AE006914; PIDN: AAL03618.1; PID: g15620202; GSPDB: GN00173
C; Genetics:
A; Gene: comp
C; Superfamily: nrfE protein
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Pred. No. 1.9e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 2; Length 662
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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Best Local Similarity 62.5%;
Matches 5; Conservative
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RX MEDLINE=22388257; PubMed=12477932;
RA MEDLINE=2388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altaner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altachul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Nillalon D.K., Muzhy D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Nilting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Mislek M., Smailus D.E.,
RA Schnerch A., Schmutz J., Marra M.A.,
RA Schnerch A., Schmutz J., Marra M.A.,
RA Schnerch A. Schein J.E., Jones S.J.M., Marra M.A.,
RA Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
                    gallus gall
guillardia
homo sapien
                                                                          neisseria g
neisseria m
neisseria m
                                                                 brugia paha
                                                                                                          schizosacch
bacteriopha
            musculu
                                                    synechocyst
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUBERIA, Kidney, Lung, and Osteosarcoma;
MEDLINE=20108780; PubMed=10640805;
Adams J.C., Zhang L.,
"CDMA cloning of human muskelin and localisation of the muskelin
(MKIMI) gene to human chromosome 7q32 and mouse chromosome 6 B1/B2 by
physical mapping and FISH."
Cytogenet. Cell Genet. 87:19-21(1999).
                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
Masuho Y., Kanehori K.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
         P08553
P16053
O78441
P07197
P73505
P41959
O007813
Q9ju24
Q9ju24
Q9ju24
P19654
                                                                                                                                                                                                                    O9UL63; O9NSK4; O9NUS8;
28-FBB-2003 (Rel. 41, Created)
PFBB-2003 (Rel. 41, Last sequence update)
15-SBP-2003 (Rel. 42, Last amnotation update)
                                                                                                                                                                                                           735 AA
                                                                                                                                                      ALIGNMENTS
                                                    SYI_SYNY3
RS26_BRUPA
                                                                                                         IDII SCHPO
REPL BPP1
                              HUMAN
                                                                          NEIGO
                                                                                    NEIMA
                                                                                                RS6 NEIMB
                                                                                                                                                                                                           PRT;
                                          NEW
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                                                                                                                                                                                                           STANDARD;
845
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847
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915
988
1122
1122
122
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227
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NCBI_TaxID=9606;
                                                                                                                                                                                                           MKLN HUMAN
 Muskelin.
                                                                                                                                                                                                                                                                            MKLN1.
                                                                                                                                                                                    RESULT 1
MKLN HUMAN
 08k918 buchnera ap
09uuh4 schizosacch
09kuz2 vibrio chol
08dcl6 vibrio varln
84477 haemophilus
09c1n8 pagecurella
08712 yabrio para
08zb81 yerginia pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    salmonella
escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haemophilus
homo sapien
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                                                                                   (without alignments)
74.689 Million cell updates/sec
                                                                         December 16, 2003, 14:06:35; Search time 5.66667 Seconds
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Q42982
Q9h2c0
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089a41
P15496
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P50860
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08xdi1
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P02358
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014734
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          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                              127863 seqs, 47026705 residues
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RRPO NODAV
HMDH ASPTE
RSG BUCBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDII YEAST
RPOA MESVI
ERG3 CANGA
DHE4 PSYT1
NFM PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                        MKLN HUMAN
MKLN MOUSE
WYLA MOUSE
KV1A MOUSE
RSE BUCAP
ER25 SCHPO
ERSE VIBCH
RSE VIBCH
RSE VIBCH
RSE VABVU
RSE HARIN
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RS6_YERPE
RS6_ECOL6
RS6_ECOL1
RS6_ECOL1
NAPC_HAEIN
PTE1_HUMAN
ERG3_YEAST
4CL2_ORYSA
GAN_HUMAN
                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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TUP1_YEAST
                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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50
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                Perfect score:
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InterPro; IRR006595; CTLH.
InterPro; IRR006594; LisH.
Pfam; PF01344; Kelch; 3.
SMART; SM00668; CTLH; 1.
PROSITE; PS50897; CTLH; 1.
PROSITE; PS50896; LISH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC013703; AAH13703.1; -.
MGD; MGI:1351638; Mkln1.
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                                                                                                                                                                                                                                                                                                    tumor;
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TISSUE=Breast tumo
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469
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                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                        (By similarity).

--- SUBUNIT: Binds with the C-terminal tail of the prostaglandin EP3 receptor alpha isoform (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Contains 5 Kelch repeats.
--- SIMILARITY: Contains 1 LisH domain.
--- SIMILARITY: Contains 1 CTLH domain.
--- SIMILARITY: Contains 1 CTLH domain.
--- CANTION: Ref. 2 sequence differs from that shown due to a stop codon in position 171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 4.1;
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111 N -> Y (IN REF. 1).
408 I -> N (IN REF. 1).
436 Q -> K (IN REF. 1).
474 G -> K (IN REF. 1).
502 T -> N (IN REF. 1).
84767 MW; IA8F06FEIDE9193D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP047489; AAF06698.1; --
EMBL; AC02024; BAA92042.1; ALT_SEQ.
EMBL; BC002834; AAH02834.1; ALT_INIT.
EMBL; AL162071; CAB82407.1; --
PIR; T41173; T47173.
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CGTLH.

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InterPro; IPR006595; CTLH.
InterPro; IPR0066595; CTLH.
InterPro; IPR006594; LisH.
Pfam; PF01344; Kelch; 3.
SMART; SM00667; CTLH; 1.
PROSITE; PS50897; CTLH; 1.
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(Rel. 41, Last sequ
(Rel. 42, Last anno
[4]
SEQUENCE OF 320-735 FROM N.A.
TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.08;
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Matches 7; Conservative
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089050;
28-FEB-2003
28-FEB-2003
15-SEP-2003
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                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. MCBI_TaxID=10090;
                                                                        SEQUENCE FROM N.A.
MEDLINE=98393538; PubMed=9724633;
Adams J.C., Seed B., Lawler J.;
"Muskelin, a novel intracellular mediator of cell adhesive and cytoskeletal responses to thrombospondin-1.";
EMBO J. 17:4964-4974(1998).
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDINES-6788890; MEDINES-8141357; PubMed=6788890; MEDINES-8141357; PubMed=6788890; MedinEs-8141357; Rudikoff S., Seidman J.G., Leder P., Scharff M.D.; "Nucleic acid and protein sequences of phosphocholine-binding light
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
30S ribosomal protein S6.
RPSF OR BUSGS44.
Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.0%; Score 36; DB 1; Length 114; 100.0%; Pred. No. 3.3; 0; Mismatches 0; Indels
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40 COMPLEMENTARITY-DETERMINING-1
55 FRAMEWORK-2.
62 COMPLEMENTARITY-DETERMINING-2
94 FRAMEWORK-3.
103 COMPLEMENTARITY-DETERMINING-1
113 FRAMEWORK-4.
94 BY SIMILARITY.
114
114
117 MW; 32000BEC8B9DBE67B CRC64;
                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
If Kappa chain V-I region S107A.
Mus musculus (Mouse).
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                                                                                                                          PRT;
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HSSP, P01607; IREI.
Interpro; IPR003106; Ig-like.
InterPro; IPR003066; Ig-MHC.
InterPro; IPR003596; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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                                                                                                                        STANDARD;
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594 LHKVHYL 600
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                        KV1A MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RS6 BUCAP
Q8K918;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       chains."
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                                                                                RESULT 4
KV1A MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
RS6_BUCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                    셤
                                                                                                                                          OS BELL BLOOK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         minimus to the strategies of the prostagland of the prostagland in EP3

-!- FUNCTION: Acts as a mediator of cell spreading and cytoskeletal responses to the extracellular matrix component thrombospondin 1 [By similarity].
-!- SUBUNIT: Binds with the C-terminal tail of the prostaglandin EP3 receptor alpha isoform.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBLIARITY: Contains 5 Kelch repeats.
-!- SIMILARITY: Contains 1 LisH domain.
-!- SIMILARITY: Contains 1 LisH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND INTERACTION WITH EP3-ALPHA.
MEDINTE-20462961; PubMed=11006128;
MEDINTE-20462961; PubMed=11006128;
MESEGAWA H., Katch H., Fujita H., Mori K., Negishi M.;
"Receptor isoform-specific interaction of prostaglandin EP3 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                     80.0%; Score 40; DB 1; Length 735; 100.0%; Pred. No. 4.1; ive 0; Mismatches 0; Indels
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7B0C8D2CB8C242AA CRC64;
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0
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                          735 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%; Score 40; DB
ilarity 100.0%; Pred. No. 4.1
Conservative 0; Mismatches
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KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006595; CTLH.
InterPro; IPR006652; Kelch_rep.
InterPro; IPR006594; LisH.
Pram; PF01344; Kelch; 3.
SMART; SM00668; CTLH; 1.
SMART; SM00667; LisH; 1.
  84877 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB046442; BAB21439.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50897; CTLH; 1. PROSITE; PS50896; LISH; 1.
                                       Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                         594 LHKVHYL 600
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Best Local Similarity
'-hea 7; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat
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  735 AA;
                                                                                                                     2 ГНКУНУГ 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              muskelin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kelch repeat;
                                                                                                                                                                                                                                                                                                                                                                              MKLN1 OR MSK.
  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                         Muskelin
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REPEAT
REPEAT
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SO THE FEET WAS A PROPERTY OF THE PROPERTY OF 
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Mod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Rodouvos U., Peat N., Hayles J., Basham D., Bowaman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huche E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Nooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neil S., Saures R., Seeger K., Sharp S.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.', Warren T., Whitehead S.,
Woodward J., Volckaert G., As Walsh S.', Warren T., Whitehead S.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
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                                                                                                                               MEDLINE=22084549; PubMed=12089438; Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S., Tamas I., Klasson L., Canbaeck B., Moran N.A., Andersson S.G.E.; Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; "50 million years of genomic stasis in endosymbiotic bacteria."; Science 296.2376-2379 (2002).
-!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
                                                                                                                                                                                                                                                                                                                                                        SIMILARITY). - :- SIMILARITY: BELONGS TO THE SGP FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP, MF 00360; -; 1.
InterPro; IRR00529; Ribosomal S6.
Fran, PF01250; Ribosomal S6; 1.
ProDom; PD003809; Ribosomal S6; 1.
ProSFAMS; TIGR00166; S6; 1.
PROSITE; PS01048; RIBOSOMAL S6; 1.
Ribosomal procesin; RRNA-binding; Complete proteome.
SEQUENCE 113 AA; 13501 MW; DE1D9286344C1BEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
ERG25 OR SPAC630.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE014128; AAM68083.1; -.
   Enterobacteriaceae; Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.5.
S; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 LHKAHYIL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LHKVHYLV 9
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                                                                                                      FROM N.A.
                                          NCBI_TaxID=98794;
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                                                                                                                                                                                                                                                                                                                                                 similarity)
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Q9UUH4;
                                                                                                          SEQUENCE
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       PALE REPAREMENT OF THE PROPERTY OF THE PROPERT
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MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shpakovski G.V. Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-886(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: Ergosterol biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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PIR; T38986; T38986.
GeneDB SPombe; SPAC630.08c; -.
InterPro; IPR006089; Sterol_desat.
InterPro; IPR006088; Sterol_desatur.
Pfam; PF01599; Sterol_desat; 1.
Sterol_biosynthesis; Oxidoreductase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                            methyl groups of 4,4-dimethylzymosterol (By similarity)
-!- COFACTOR: Iron (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.0%; Score 35; DB 1; Length 300; 71.4%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and/or be involved in metal ion binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 HISTIDINE BOX-1.
171 HISTIDINE BOX-2.
257 HISTIDINE BOX-3.
35802 MW; AARCZ603D35DF331 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSG_VIBCH STANDARD; PRT; 122 AA. 09MUZ2.

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
30 ribosomal protein S6.

RPSF OR VC0366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 14;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.4%;
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 1
167 1
251 2
300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 FIHKVHH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fransmembrane; Iron.
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Pfam; PF01250; Ribosomal S6; 1.
ProDom; PD003809; Ribosomal S6; 1.
IPR000529; Ribosomal_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter J.C.;
    InterPro;
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McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                  "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                           -! - SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.0%; Score 34; DB 1; Length 122; 62.5%; Pred. No. 8.6; 1; Indels ive 2; Mismatches 1; Indels
                                                                                                                Nature 406:477-483(2000).
-!- FUNCTION: BINDS TOGETHER WITH S18 TO 16S RIBOSOMAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF 00360; -; 1.
InterPro; IPR00529; Ribosomal_S6.
InterPro; IPR00529; Ribosomal_S6; 1.
ProDom; P0003809; Ribosomal_S6; 1.
TIGRFAMS; TIGR00166; S6; 1.
FROATE; PS01048; RIBOSOMAL_S6; 1.
Ribosomal protein; rRNA-binding; Complete protecme.
SEQUENCE 122 AA; 14249 MW; 4BA3DB6BIFDDBA01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 30S ribosomal protein S6. RPSF OR VV11387.
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                                                                                                                                                             (BY SIMILARITY)
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SEQUENCE FROM N.A.
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                                                                                                 cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Puhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: MODIFIED POST-TRANSLATIONALLY BY THE ADDITION OF C-TERMINAL GLU RESIDUES BY THE RIMK ENZYME (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
-:- FUNCTION: BINDS TOGETHER WITH S18 TO 16S RIBOSOMAL RNA
                                                                                                                                                        Score 34; DB 1; Length 123; Pred. No. 8.6;
                                                                                                                                                                                                                       Indels
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PROSITE; PS01048; RIBOSOMAL S6; 1.
Ribosomal protein; rRWA-binding; Complete proteome.
SEQUENCE 125 AA; 14484 MW; A3804A2FEFBEBERC CRC64;
                                                                                                123 AA; 14301 MW; FCA3C5582FDA3C03 CRC64;
                                                                       Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RPSF OR RPS6 OR HI0547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 AA
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PROSITE; PS01048; RIBOSOMAL S6; 1.
Ribosomal protein; FRNA-binding; C
SEQUENCE 123 AA; 14301 MW; FCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECURICE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542806;
                                                                                                                                                            68.0%;
62.5%;
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                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                          54 LHKAHYVL 61
                                                                                                                                                            Query Match
Best Local Similarity
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Length 125;

DB 1;

68.0%; Score 34;

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Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=632;
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Matches
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             Gaps
                                                                                                                                                                                                                                                                                   May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- FUNCTION: BINDS TOGETHER WITH S18 TO 16S RIBOSOWAL RNA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS
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                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
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Vibrio parahaemolyticus.

Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae; Vibrio.

Vibrionaceae; Vibrio.

[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 125; Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGRO0166; S6; 1.—
PROSTIR; PSO1048; RIBOSOWAL S6; 1.
Ribosomal protein; TRNA binding; Complete proteome.
SEQUENCE 125 AA; 14505 MW; 102C842FD3FF7736 CRC64;
             ..
                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Solosomal procein S6.
RPSF OR RPSG OR PM1180.
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                                                                                                                 125 AA
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             Mismatches
  Pred. No.
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InterPro; IPR000529; Ribosomal S6.
Pfam; PF01250; Ribosomal S6; 1.
ProDom; PD003809; Ribosomal S6; 1.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RS6_VIBPA STANDARD; E Q87L72; 15-SEP-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE006158; AAK03264.1; -.
                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
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62.5%;
 62.5%;
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           5; Conservative
                                                                                                                 STANDARD;
                                                                                                                                                                                              Pasteurella multocida
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LHKAHYVL 61
                                                      54 LHKAHYVL 61
                                  2 ГНКУНУЦУ 9
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Best Local Similarity
Matches 5; Conserv
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RS6 VIBB

AC RS6 VIBB

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STRAIN=CO-92 Biovar Orientalis;
MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin M., Holtroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Shelton J., Stevens K., Whitehead S., Barrell B.G.,
Nature 413:523-527(2001).
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MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                               similarity).
-!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.0%; Score 34; DB 1; Length 129; 62.5%; Pred. No. 9.1; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRUDA, MP 00360; -; 1.
PROSITE; FS01048; RIBOSOMAL S6; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBZBB1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
SES ribosomal protein S6.
RPSF OR YPO3539 OR Y0645.
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J. Bacteriol, 184:4601-4611(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
0-92 / Biovar Orientalis;
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tes 5; Conservative
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54 LHKAHYVL 61
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SEQUENCE FROM N.A.
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Q8XG88;
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Matches
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RS6_SALTY
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                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=210.74935; PubMed=11206551;
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Apofack E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
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Enterobacteriaceae, Escherichia.
NCBL_TaxID=217992, 83334, 623;
                          similarity).
-!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOWAL PROTEINS.
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Binds together with $18 to 16S ribosomal RNA (By
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InterPro; IRR006529; Ribosomal S6.
Promom, PR01250; Ribosomal S6; 1.
Prodom, PR01309; Ribosomal S6; 1.
TIGRFAMS; TIGR00166; S6; 1.
PROSITE; PS01048; RIBOSOMAL S6; 1.
Ribosomal protein; FRNA-binding; Complete proteome. SEQUENCE 130 AA; 15008 MW; 7897E436DD1FA562 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
30S ribosomal protein S6.
30S ribosomal protein S6.
Escherichia coli 06,
Escherichia coli 06,
Escherichia coli 0157:H7, and
                                                                                                                                                                                                                                                                                                           EMBL; AJ414157; CAC92768.1; -.
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54 LHKAHYVL 61
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Best Local Similarity
Matches 5; Conserv
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  FUNCTION:
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RS6 ECOL6
AC QRXDI1,
DT 28-FEB-2003
DT 28-FEB-2003
DE 30S ribosom
GN RPSP OR C52
OS Bacherichia
OS Bscherichia
OS Bs
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                               MEDLINE=21156231, PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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-!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                0157:H7 and genomic comparison with a laboratory strain K-12.", DNA Res. 9:11-22(2001).
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REMBL; AE005652; AAG59396.1; --
REMBL; AE005688; BAB38599.1; --
REMBL; AE015442; AAN45771.1; --
REMBL; AE01542; AAN45771.1; --
REMBL; AE01542; AAN45771.1; --
REMBL; AE01542; AAN45771.1; --
REMBL; AE0154; REG.
REMBL; AE0260; --
REMBL;
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SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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RPSF OR STM4391 OR STY4747 OR T4442.
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NCBI TaxID=602, 601;
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21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
15-SEP-2003 (Rel. 42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deng W., Liou S.R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
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                             PERCIES. Typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERCIES. 1797bi; STRAIN=CT18; MEDLINE=2153494; PubMed=11677608; MEDLINE=2153494; PubMed=11677608; MEDLINE=2153494; PubMed=11677608; MEDLINE=2153494; PubMed=11677608; MEDLINE=2153494; PubMed=11677608; MEDLINE=2153494; PubMed=1167; Medle M.T.G., Sebahia M.J. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis R.M., Dowd L., White N., Farrar J., Cronin A., Larsen T.S., Leather R., Hien T.T., Holloyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G.; Michehead S., Barrell B.G.; Monilete genome sequence of a multiple drug resistant Salmonella enterica servorar Typhi CT18.";
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-!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
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-!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
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ProDom; PD003809; Ribosomal_S6; 1.
TIGRPAMs; TIGRO166; S6; 1.
PROSITE; PS01048; RIBOSOMAL S6; 1.
Ribosomal protein; RRNA-binding; Complete proteome.
SEQUENCE 131 AA; 15173 MW; 54974D6342C21362 CRC64;
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2; Mismatches
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InterPro; IPR000529; Ribosomal_S6.
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135 AA

PRT;

STANDARD;

RESULT 15 RS6\_ECOLI ID RS6\_ECOLI AC P02358;

||| ||:: 54 LHKAHYVL 61

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Hitz H., Schaefer D., Wittmann-Liebold B.;
"Determination of the complete amino-acid sequence of protein S6 from
"Intermination of the complete amino-acid sequence
the wild-type and a mutant of Escherichia coli.";
Eur. J. Biochem. 75:497-512(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           properties of proteins encoded
                                                                                                                                                                SEQUENCE OF 1-131 FROM N.A.
MEDLINE-86310297; PubMed=3528756;
Schnier J., Kitakawa M., Isono K.;
"The nucleotide sequence of an Bscherichia coli chromosomal region containing the genes for ribosomal proteins S6, S18, L9 and an open
                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98263247; bubMed=9600841;
Wilkins M.R., Gasteiger E., Tonella L., Ou K., Tyler M.,
Sanchez J.-C., Gooley A.A., Walsh B.J., Bairoch A., Appel R.D.,
Williams K.L., Hochetrasser D.F.,
"Protein identification with N and C-terminal sequence tags in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASS SPECTROMETRY.
STRAIN-EX.2 / ATCC 25404;
MEDLINE=99195679; Wand=10094780;
Arnold R.J., Reilly J.P.;
"Observation of Escherichia coli ribosomal proteins and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-11.
STRAIN=K12 / W1110;
Pasquali C., Sanchez J.-C., Ravier F., Golaz O., Hughes G.J.,
Frutiger S., Paquet N., Wilkins M., Appel R.D., Bairoch A.,
Hochetrasser D.F.,
                                                                                                                                                                                                                                                                                                                                                                                   "Analysis of the Escherichia coli genome VI: DNA sequence of region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                    MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                posttranslational modifications by mass spectrometry.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99085675; PubMed-9868784; Wathinger V.C., Rumphery-Smith I.; Manlager F. Rumphery-Smith I.; Manla genes/gene-products in Escherichia coli K-12."; FEMS Microbiol. Lett. 169:375-382(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1994) to the SWISS-PROT data bank.
   15-SEP-2003 (Rel. 01, Last sequence update)
308 ribosomal protein S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed prop
in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313 (1997).
                                                                                                                                                                                                                                                                     Mol. Gen. Genet. 204:126-132(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-12.
STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K;
MEDLINE=77225229; PubMed=328274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roteome projects.";
. Mol. Biol. 278:599-608(1998).
                                                                                                                   Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-131 FROM N.A.
                                                                                                                                                                                                                                                                                                                  / MG1655;
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STRAIN=K12 / W3110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-20.
                                                                                   Escherichia coli
                                                                                                                                                                                                                                                     reading frame."
                                                                                                                                    NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                       Blattner F.R.;
                                                                RPSF OR B4200
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                  NAL. SERUCE. BIOL. 9:750-755 (2002).

-I. FUNCTION: BINDS TOGETHER WITH $18 TO 16S RIBOSOMAL RNA.

-I. FUNCTION: BINDS TOGETHER WITH $18 TO 16S RIBOSOMAL RNA.

-I. FUNCTION: BINDS TOGETHER WITH $18 TO 16S RIBOSOMAL RNA.

OF CARBOXYL-TERMINAL GLUTAMIC ACID RESIDUES, WERE ISOLATED. THE SEQUENCE SHOWN IS FORM $6-6, WHICH IS THE LONGEST. THE FIRST 2 GLU ARE ENCODED BY THE RAPE FORD, THE OTHER GLU ARE ADDED POST-

TRANSLATIONALLY BY THE RIMK ENZYME.

-I. MASS SPECTROMETRY: WW-15187. 2, METHOD-WALDI; RANGE=1-131.

-I. SIMILARITY: BELONGS TO THE $6P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01250; Ribosomal_S6; 1.

Prodom; PD03809; Ribosomal_S6; 1.

TIGREAMS; TIGRO0166; S6; 1.

PROSITE; PS01048; RIBOSOMAL_S6; 1.

Ribosomal protein; rRNA-binding; 3D-structure; Complete proteome.

CHAIN 132 SOF RIBOSOMAL PROTEIN S6, NON-MODIFIED ISOFORM.

CHAIN 135 RIBOSOMAL PROTEIN S6, FULLY MODIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                         Tung C.-8., Joseph S., Sanbonmatsu K.Y.; "All-atom homology model of the Escherichia coli 30S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.0%; Score 34; DB 1; Length 135; ilarity 62.5%; Pred. No. 9.5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G -> T (IN REF. 4).
G -> A (IN REF. 4).
F4CC629711C1FD0E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X04022; CAA27652.1; -...
EMBL; U14003; AAA97096.1; -...
EMBL; AE000491; AAC77157.1; -...
FDB; IMSG; 09-UUL-02.
SWISS-2DPAGE; P02358; COLT.
ECOZDBASE; O1014.7; ETH EDITION.
ECOZDBASE; CO14.8; ETH EDITION.
ECOZDBASE; CO14.8; ETH EDITION.
ECOZDBASE; CO15.3; ETH EDITION.
ECOZDBASE; CO15.3; ETH EDITION.
HWARP; MF 00360; -: 1.
InterPro; IPR000529; Ribosomal_S6.
                                                            MEDLINE=22239879; PubMed=12244297;
Anal. Biochem. 269:105-112(1999).
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20 20 G
135 AA; 15703 MW;
                                          3D-STRUCTURE MODELING
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Best Local Similarity
Matches 5; Conserv
                                                                                                                   subunit.";
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Db 54 iHKAHYVI 61 Search completed: December 16, 2003, 14:15:16 Job time : 6.66667 secs

2 LHKVHYLV 9

8

Run

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Q8rvy8 brassica ca
Q8s9c1 brassica ca
Q8sv20 brassica ca
Q8rvy9 brassica ca
Q8rd4 staphylococ
Q8td7 homo sapien
O0153 caenorhabdi
Q9tty4 canis famil
Q9tty4 canis famil
Q4td36 ciona intes
Q92p2 rickettsia
Q8td39 homo sapien
Q81d39 homo sapien
Q81d48 babesia bov
Q92ht rickettsia
Q8dc16 vibrio vuln
Q8dc16 vibrio vuln
Q8eah2 shewanella
                                                                                                                                                                                                  Q9bt16 homo sapien
Q9cwl2 mus musculu
Q9uq17 homo sapien
Q9y977 aeropyrum p
Q8s0y4 salmonella
Q8n798 homo sapien
                                                                                                                                                                                     Q94ct9 oryza sativ
Q8r9b9 thermoanaer
                         Q8s9c2 brassica ol
28i077 drosophila
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio,
NCBI_TaxID=7958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%; Score 40; DB 13; Length 729; 100.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams J.C., Zaromytidou A.-I.; "Zebrafish muskelin from cDNA."; "Zebrafish muskelin from cDNA."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF418017; AAN12664.1; -SEQUENCE 729 AA; 84376 MW; DFB3672F5D0AE16F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                     729 AA
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                        Q8S9C2
Q8RVY8
Q8S9C1
Q8RVZ0
Q8RVY9
Q8CND4
                                                                                                              044236
Q92GP2
Q8TDJ9
Q8NGZ7
                                                                                                                                                 027448
092HR4
08DCL6
08EAH2
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Q8R9B9
Q9BT16
Q9CWL2
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Q9Y977
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09TTY4
08TDJ8
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01-JUN-2002 (TrEMBLrel. 21, C
01-JUN-2002 (TrEMBLrel. 21, L
01-MAR-2003 (TrEMBLrel. 23, L
Chitin synthase V.
CHS5.
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
1078
1084
1673
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92
92
182
182
347
457
650
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Muskelin,
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QBAYJS
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Q8TGV2
GETTT
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Q8K468 Glostridium
Q94K11 arabidopsis
Q9K4f0 mus musculu
Q33227 arabidopsis
Q92cr5 listeria in
Q8777 listeria in
Q8777 listeria ac
Q92cm1 rickettsia
Q81ja8 plasmodium
Q94km2 drosophila
Q94km2 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O8tgv2 exophiala d
O9gkx9 sus scrofa
O77563 sus scrofa
O8t2d3 dictyosteli
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                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                         2003, 14:09:45; Search time 25 Seconds (without alignments) 92.899 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
        GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                         830525 segs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                         using sw model
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Q8K4F0
O23227
Q92CR5
Q8Y7X7
Q9ZCM1
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Q8TGV2
Q9GKX9
O77563
Q8T2D3
Q8K4E4
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_bhage:*
sp_plant:*
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sp_vertebrate:*
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sp_bacteriap:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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Maximum DB seq length: 200000000
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Match Length DB
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                                         protein search,
                                                           December 16,
                Copyright
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GTRAIN-AX4;
Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Gloeckner G., Baumgar L., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and Analysis of Chromosome 2 of Dictyostelium.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC115613; AANIO762.!
InterPro: IPR003006; Ig_MHC.
InterPro: IPR00648; Oxysterol_BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                            Meljerink B., Voegeli P., Stranzinger G.;
Meljerink B., Voegeli P., Stranzinger G.;
"The putative porcine blood group A transferase cDNA.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF050177; AAC68840.1;
INTERPRO'S GIVO trans 6.
Pfam, PF03414; Glyco_trans 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al protein. 439 AA; 49590 MW; 65F0C94E40E4AAD9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8T2D3 PRELIMINARY, PRT, 439 AA.
Q8T2D3;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2003 (TrEMBLrel. 21, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 49.6 kDa protein.
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Last sequence update)
Last annotation update)
                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                   Putative blood group A transferase.
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PROSTTE, PS00290, IG_MHC, 1.
Hypothetical protein.
SEQUENCE 439 AA, 49540 MM.
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nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel, 22, 01-MAR-2003 (TrEMBLrel, 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 55.6
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                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                             Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase.
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Q8K4E4
ID Q8K4I
AC Q8K4I
DT 01-00
DT 01-00
DT 01-00
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                                                                                                                                            SEQUENCE FROM N.A.

A Liu H., Szaniszlo P.J.;

RT "Cloning and Characterization of a Class V Chitin Synthase Gene
Liu H., Szaniszlo P.J.;

RT (WCHESS) of Wangiella (Exophiala) dermatitidis, A Model Dematiaceous

RT Pathogen of Humans.";

RT PATHOGEN OF HALTORON.1 - .

DR PEMBL, AF69116, AALTORON.2 | . .

DR InterPro; IPR001199; Cyt B5.

DR InterPro; IPR00169; myosin head.

DR Pfam; PF00173; heme 1; 2.

DR Pfam; PF00063; myosin head; 1.

DR Pfam; PF00063; myosin head; 1.

DR Pfam; PF00063; Myosin head; 1.

DR Probom; PD006612; Cyt B5; 1.

DR Probom; PD006612; Cyt B5; 1.

DR SMART; SM00242; MYSC; 1.

DR SMART; SM00242; MYSC; 1.
                           Eukāryota; Fungi; Ascomycotā; Pezizomycotina; Chaetothyriomycetes;
Chaetothyriales; Herpotrichiellaceae; mitosporic Herpotrichiellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mammatian ABO genes: Murine AB gene encodes a glycosyltransferase with both A and B transferase activity and porcine O gene is a null sallel due to a major chromosomal aberration."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, ABO41040; BAB20561.1; -...

PFam; PP03414; Glyco_transf_6; 1...

Transferase.

NON TER 152 152
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Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1885;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.0%; Score 39; DB 3; Length 188
85.7%; Pred. No. 1.1e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
A transferase (Fragment).
   Exophiala dermatitidis (Wangiella dermatitidis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 AA.
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1; Mismatches
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Mammalia; Eutheria;
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Matches 7; Conserv
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FLHEVDYLV
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Best Local Similarity
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                                                                                                                   NCBI TaxID=5970;
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RESULT 3 Q9GKX9

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Score 36;
Pred. No.
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Interpro; IPR001089; AB hydrolase.
Interpro; IPR001089; Bpox hydrolase.
Interpro; IPR000379; Ser estrs_site.
Pfam; PP00561; abhydrolase; 1.
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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PRINTS; PR00412; EPOXHYDRLASE.
                72.0%;
75.0%;
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             Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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Matches 5; Conservative
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                                                                                                                                                 22 LHYVHYLI 29
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                                                                                                     2 LHKVHYLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
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Q8K4F0;
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Q8K4F0
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                                                                                                                                                                                                                                                      "TLISAI (PTA1) activation antigen implicated in T cell differentiation and platelet activation is a member of the immunoglobulin superfamily exhibiting distinctive regulation of expression."; J. Biol. Chem. 272:21735-21744 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jin B., Zhang X., Li D., Ouyang W., Jia W., Chen L., Xie X., Ning S., Zhang Y.; "Gene cloning and characterization of mouse platelet and T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Tian F., Li D., Xia H., Liu X., Jia W., Sun C., Sun K., Jin B.; "Isolation of cDNAs encoding gibbon and monkey platelet and T cell activation antigen 1 (PTA1)."; DNA Seq. 10:155-161(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                    Mus musculus (Mouse).
Wakaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium perfringens.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                          MEDLINE=97413766; PubMed=9268302; Sherrington P.D., Scott J.L., Jin B., Simmons D., Dorahy S.J., Lloyd J., Brien J.H., Aebersold R.H., Adamson J., Zuzel M., Burns G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 11; Length 187;
Pred. No. 43;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activation antigen I (PTA1/CD226).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 74F421198; AAN04296.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFam; PF00047; ig; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 187 AA; 21393 MW; 70D29BE21927ACE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60F81BD7DFD6C973 CRC64;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein CPE1366.
Platelet and T cell activation antigen 1 isoform 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           flesh-eater.";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP003190; BAB81072.1;
Hypothetical protein; Complete proteome.
SEQUENCE 250 AA; 29634 MW; 60F81BD7DFD6C973
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                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/C;
MEDLINE=20112343; PubMed=10647817;
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62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 YLHRVHFL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=13 / Type A;
PubMed=11792842;
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Best Local Similarity
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                                                                                                                              SEQUENCE FROM N.A.
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                                                                                     NCBI_TaxID=10090;
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NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8XKMB;
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Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Sakurai T., Theologis A., Davis R.W.;
Submitted (Apr.-2001) to the EMBL/GenBank/DBJ databases.
Submitted (Apr.-2001) to the EMBL/GenBank/DBJ databases
OF EPOXIDES (ALKENE OXIDES, OXIRANES) AND ARENE OXIDES TO LESS
REACTIVE AND MORE WATER SOLUBLE DIHYDRODIOLS BY THE TRANS ADDITION
OF WATER (BY SIMILARITY: AN EDOXIDE + H(2)O = A GLYCOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last amoutation update)
UNKNOWN protein (EC 3.3.2.3) (Epoxide hydrolase).
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                   Gaps
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Jin B., Zhang X., Li D., Ouyang W., Jia W., Chen L., Xie X., Ning S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Platelet and T cell activation antigen 1.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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DB 16; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 321;
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                321 AA.
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2; Mismatches
                                                                      1; Mismatches
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Hypothetical protein; Aromatic hydrocarbons catabolism;
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Q92CR5
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Brover V. Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
Feldmann K.;
Feldmann K.;
Submitted Kar-2002 to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: BIOTRANSFORMATION BAZYME THAT CATALYZES THE HYDROLYSIS
-- FUNCTION: BIOTRANSFORMATION BAZYMES AND ARRNE OXIDES TO LESS
REACTIVE AND MORE WATER SOLUBLE DIHYDRODIOLS BY THE TRANS ADDITION
OF WATER (BY SIMILARITY).
-- CATALYTIC ACTIVITY: AN EPOXIDE + H(2)O = A GLYCOL.

EMBL; 299708; CABL6840.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (EC 3.3.2.3) (Epoxide hydrolase).
C7A10.830 OR AT4G36530.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                 Zhang Y.;

actioning and characterization of mouse platelet and T cell
activation antigen 1 (PTA1/CD226).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AF416990, AAN04295.1;
InterPro; IPR001599; IG.
InterPro; IPR00110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 11; Length 333;
Pred. No. 75;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bevan M., Terryn N., Vos P., Heijnen L., Mewes H.W., Sch
Chalwatzis N.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
[2]
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
PROSITE; PS0835; IG_LIKE; 2.
SEQUENCE 333 AA, 38063 MW; ACDE524D0F475C97 CRC64;
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EMBL, AV087588, AAM5130.1; --
EMBL, AV087588, AAM5130.1; --
InterPro; IPR000073, A/b hydrolase.
InterPro; IPR000639; Bpox_hydrolase.
InterPro; IPR000379; Ser_estrs_site.
Pfam, PF00561; abhydrolase; I.
PRINTS; PR00111; ABHYDROLASE.
PRINTS; PR00111; ABHYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.0%;
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Query Match
Best Local Similarity 62.5%,
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Genome Biol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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76 YLHRVHFL 83
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SEQUENCE FROM N.A.
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NCBL_TaxID=3702;
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Baquero F., Frangeul L., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetcuani F., Couve B., de Daruvar A., Dehoux P.,
Butian K.-D., Fsihi H., Garcia-del Portillo F., Durant L., Dussurget O.,
Bntian K.-D., Fsihi H., Gomez-Lopez N., Hain T., Hauf U., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kuraptat G.,
Madueno E., Mattcurnam A., Mata Vicente J., Ng B., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Warquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                            Length 378;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein lmol142.
Limol142.
Listeria monocytogenes.
Bacteria, Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TAXID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBL_TaxID=1642;
                                                                                                             0; Indels
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Listilist, LIN01106; -.
Listilist, LIN01106; -.
LinterPro; IPR001450; 4F48. ferredoxin.
InterPro; IPR00149; Complex1.51K.
Pfam; PF01512; Complex1.51K; 1.
Pfam; PF00037; fer4; 1.
PROSITE; PS00198; 4F48. FERREDOXIN; 1.
Hypochetical protein; Complete proteome.
SEQUENCE 454 AA; 49918 MW; 068B138B9213B239 CRC64;
Decoxification, Hydrolase.
SEQUENCE 378 AA, 41906 MW; 8D1FB39D5410E818 CRC64;
                                                                                                                                                                                                                                                                                                                                   Q92CR5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein linl106.
                                                            Score 36; DB 10;
Pred. No. 85;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                   454 AA
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                                                                                                                                                                                                                                                                                                                   PRT;
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STRAIN=CLIP 11262 / Serovar 6a;
PubMed=11679669;
                                                                 72.0%;
                                                                                      71.48;
                                         Query Match
Best Local Similarity 71.4%,
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239 YLHKLHY 245
                                                                                                                                                                                   ||:||:|
89 HKIHYVV 95
                                                                                                                                                         3 HKVHYLV 9
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01-MAR-2003 (TrEMBLrel. 23, Created)
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526 FQHRIHYL 533
                 500 LHNVHYLL 507
2 LHKVHYLV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FLHKVHYL 8
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Matches 5; Conserv
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                                                                                                                                                                                                          NCBI TaxID=36329;
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                                                               RESULT 14
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                                             Character P., Parageul L., Buchrieser C., Rusnick C., Amend A.,

Adlaser P., Frangeul L., Buchrieser E., de Darnvar A., Dehoux P.,

Adrabit A., Chetouani F., Couve B., de Darnvar A., Dehoux P.,

Domann E., Dominquez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

Adulier L., Goebel W., Gomez-Lopez N., Hain T., Hauf U., Jackson D.,

Jones L.-M., Kaerst U., Kaerst U., Krust F., Kunst F.,

Madueno E., Maitournam A., Mata Vicente J., Ng B., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoss N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

Comparative genomics of Listeria species.",

Science 294:849-852(2001).

EMBL, AL591978; CAC99220.1; -.

EMBL, AL591978; CAC99220.1; -.

Entitist; LM001142; -.

EMBL, AL591078; Complex1 51K.

Ffam; PF00137; fer4; I.

PROSITE; PS00198; 4Fe4S FERREDOXIN; 1.

PROSITE; PS00198; 4Fe4S FERREDOXIN; 1.

SEQUENCE 454 AA, 49891 MW; 006AD8FSC732B44B CRC64;
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Rickettsiaceae; Rickettsieae; Rickettsia.
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Pred. No. le+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 670;
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75.0%; Pred. No. 1.5e+02;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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MAX-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Cytochrome C-type biogenesis protein CCMF (CCMF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mature 396:133-140(1998).

EMBL, AJ235273; CAA15139.1; -.

InterPro; IPR002541; CYtC asm.

InterPro; IPR003567; Cyt c biog.

InterPro; IPR000276; GPR Rhodpsn.

Pfam; PF01578; CytC asm; I.

PRINTS; PR01410; CCBIOGENESIS.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

Complete protecome.

SEQUENCE 670 AA; 76847 MW; 2703AlAC44F9EB
                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
          SEQUENCE FROM N.A.
STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                      72.0%;
71.4%;
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 71.4 es 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                        :|||:||
239 YLHKLHY 245
                                                                                                                                                                                                                                                                                                                                                                                                        1 FLHKVHY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitochondria."
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09ZCM1;
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                                                                                                                                                                                                                                                                                                                                                                                datches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallon S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Worferdden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Berkeley;
MEDLINE-20195006; PubMed=10731132;
Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                          Přio 0290.
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%; Score 36; DB 5; Length 702
62.5%; Pred. No. 1.6e+02;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AE014833, AAN35487.1, -.
Hypothetical protein.
SEQUENCE 702 AA, 82907 MW, 37D1DDB57A12AE6B CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
CG8202 protein.
                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein.
702 AA.
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Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Charty J.M., Cabley S., Dahlke C., Davenport L.B., Davies P.,

de Pablos B., Delcher A., Deng Z., Mays A.D., Deev I., Dietz S.M.,

Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA, Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Felschmann W.,

RA, Broiler C., Gabrielian A.E., Garg N.S., Galbart W.M., Glasser K.,

RA, Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA, Hostin D., Houston K.A., Howland T.J., Mernhison J.A., Ketchum K.A.,

RA, Arinis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA, Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA, Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lini Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA, Marklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA, Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA, Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA, Wang Z.-Y., Wassarman D.A., Weinsenbach J.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA, Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA, Chor S., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA, Schor S., Chong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

RA, Chor S., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA, Weiber R., Shong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,

Ra, Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Rainer Sequence of Diosophila melanogaster.";

Ry Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subjected From. N. H. Saples M. D., Kronmiller B., Wan K. H., Holt R. A., A Calniker S. B., Adams M. D., Amanatides P. G., Brandon R. C., Rogers Y., Branson C., An H., Baldwin D., Banzon J. Beeson K. Y., Busam D. A., Carleson J. M., Center A., Champe M., Davenport L. B., Dietz S. M., Dodson K., Dorsett V., Doup L. E., Doyle C., Dresnek D., Farfan D., A Ferriera S., Frise E., Galle R. F., Garg N. S., George R. A., Gonzalez M., Houck J., Hoskins R. A., Hostin D., Howland T. J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., A McIntosh T. C., Moy M., Murphy B., Nelson C., Nelson K. A., Numoo J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., A Milliams S. M., Zaveri J. S., Puri H. W., Vinter D., Wonter D., Suputted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smuthak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB003680; AAF54212; -. Flybase; FBGN037622; CG202. SEQUENCE 716 AA, 82149 MW; 4DB233CE393C5704 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Gaps

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72.0%; Score 36; DB 5; Length 716; 71.4%; Pred. No. 1.6e+02; ative 2; Mismatches 0; Indels

Conservative

Local Similarity nes 5; Conserv

Matches

Query Match

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622 FIHKVHF 628
1 FLHKVHY 7
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Search completed: December 16, 2003, 14:18:03 Job time : 27 secs 1179, Ap 6, Appli 20, Appl 6, Appli

Sequence Seguence

31, Appl 31, Appl 6, Appli 6035, Ap 20, Appl 77, Appl 20307, A

Sequence Seq Sequence Sequence Sequence

5293, Ap 26757, A 19630, A 18540, A 26961, A

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ALIGNMENTS
                                                                                                                                                                                                                                         Sequence 2, Application US/08446855A Patent No. 5849573 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 74.5
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|| ||||
|168 KYFKKHGFS 1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KHFKPHGFS
TOPOLOGY:
                                                                                                                                                                                                                                    US-08-446-855A-2
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 RESULT 1
 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Appli
Sequence 1, Appli
Sequence 10, Appli
Sequence 5331, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 25132, A
Sequence 20, Appl
Sequence 6483, Ap
Sequence 6483, Ap
Sequence 611, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 380, Appl
Sequence 280, Appl
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Appli
Appli
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                                                            December 16, 2003, 14:11:00 ; Search time 12.3333 Seconds (without alignments) 30.875 Million cell updates/sec
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Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
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                                                                                                                                                                                                                                                                                      'cgn2_6/ptodata/1/iaa/5A COMB.pep:*
'cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
'cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
'cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
'cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
'cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-425-679E-10
US-09-107-532A-5331
US-07-727-814B-2
US-08-828-614-2
US-08-828-59-2
US-09-356-197-6
US-09-636-077A-15
US-09-525-991A-19828
US-09-325-991A-25132
US-09-328-355-6483
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US-08-868-458-2
US-09-252-991A-30355
US-09-012-710-11
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                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-446-855A-2
US-09-150-741-2
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                                                                                                                                                                        328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                Issued Patents AA:*
                                                                                                   US-09-870-089B-13
55
                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                             Length DB
                                                                                                                         1 KHFKPHGFS 9
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                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                           Sequence:
                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                Database
                                                                Run on:
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No.
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APPLICANT: Stewart, Thomas S
APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: Plores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Phosphate synthetase II
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.5%; Score 41; DB 2; Length 2391; 77.8%; Pred. No. 39; 1; Indels tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                   COUNTER TEACH TO THE COMPUTER READABLE FORM:

MEDIUM TYPE: —Toppy disk
COMPUTER. —Toppy disk
SOFTWARE: PatentIn Release #1.24
SOFTWARE: PatentIn Release #1.24
SOFTWARE: PatentIn Release #1.24
SOFTWARE: PatentIn Release #1.24
APPLICATION DATE: 06-Jul-1995
CLASSIFTATION NUMBER: US,009
REFERENCE/DOCKET NUMBER: 29.00
REFERENCE/DOCKET NUMBER: 29.09
REFERENCE/DOCKET NUMBER: 47-80
TELEPAX: 703-816-4100
TELEFAX: 703-816-4100
TELERGTH: 2391 amino acide
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5331, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: <Unknown>
Sequence 10, Application US/09425679E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 5331:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.3%;
Best Local Similarity 83.3%;
Matches 5; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Equus caballus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 HFRPHG 105
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                                                                             Sequence 2. Application US/09150741

Parent No. 6183996

GRNERAL INFORMATION:

APPLICANT: Stewart et al.

ITILE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate

Patent No. 6183996

ITILE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate

Patent No. 6183996

ITILE OF INVENTION: Synthetase II

FILE REFERENCE:

CURRENT FILING DATE: 1998-09-10

EARLIER APPLICATION NUMBER: D10380

EARLIER PILING DATE: 1992-12-16

EARLIER APPLICATION NUMBER: A093/00617

EARLIER APPLICATION NUMBER: 08/446,855

EARLIER PILING DATE: 1995-07-06

NUMBER OF SEQ ID NOS: 15

COMMUNICATION DATE: 1995-07-06

NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: McDonald, Thomas L.
APPLICANT: McDonald, Thomas L.
TITLE OF INVENTION: Serium Amyloid A Isoform from Colostrum
FILE REFERENCE: UNMC 63142
CURRENT APPLICATION NUMBER: US/09/425,679E
CURRENT FILING DATE: 1999-10-22
PRIOR PLING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/218,611
PRIOR APPLICATION NUMBER: US 60/218,611
PRIOR FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.5%; Score 41; DB 3; Length 2391; 77.8%; Pred. No. 39; 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-425-679E-8
'Sequence 8, Application US/09425679E
'Patent No. 6509444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 2391
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Equus caballus
US-09-425-679E-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1168 KYFKKHGFS 1176
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Best Local Similarity
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HFRPHG 12
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US-09-425-679E-10

RESULT 4

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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
Patent No. 6509440

GRANEAL INFORMATION:
APPLICANT: Weber, Annika L.
APPLICANT: Weber, Annika L.
TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
FILE REPERENCE: UNAMC 63142
CURRENT PILION NUMBER: US/09/425,679E
CURRENT PILION DATE: 1999-10-22
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 4; Length 110;
Pred. No. 7.5;
1; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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Patent No. 5213969
GENERAL INPORMATION:
APPLICANT: SCHUMACHER, GUNTHER
APPLICANT: BURTSCHER, Helmut
APPLICANT: APPLICANT: CLONED N-METHYLHYDANTOINASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Nikaido, Marmelstein, Kubovcik & ADDRESSEE: Marmstrong, Nikaido, Marmelstein, Kubovcik & STREET: 1725 K Street, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1288;
                                                                                                                                                               Score 37; DB 4; Length 508;
Pred. No. 39;
0; Mismatches 1; Indels
                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington D.C.
COUNTRY: United States of America
ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PARTICAL BENEVE COMPUTED SOFTWARE: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/727,814B
FILING DATE: 19910708
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1; I
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                        NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...508
SEQUENCE DESCRIPTION: SEQ ID NO: 5331:
ORIGINAL SOURCE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4021571.7
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
REFRENCE/DOCKET NUMBER: 9110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEPHONE: (202) 887-0357-
                                                                                                                                                               67.3%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1288 amino acids
TYPE: AMINO ACID
                                                                                                                                                  Query Match
Best Local Similarity 85.7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-07-727-814B-2
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97 RHKKPHNFS 105
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US-07-727-814B-2
                                      FEATURE
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US-08-258-614-2
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Sequence 2, Application US/08828596
Patent No. 5822018
GENERAL INFORMATION:
APPLICANT: Welsh, Michael J.
APPLICANT: Welsh, Michael J.
APPLICANT: Price, Magaret P.
TITLE OF INVENTION: And DNA Sequences Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                        ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,614
                                           GENERAL INFORMATION:
APPLICANT: SCHUMACHER, Gunther
APPLICANT: BURTSCHER, Helmut
APPLICANT: MOLLERING, Hans
TITLE OF INVENTION: CLONED N-METHYLHYDANTOINASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 21 571.7
FILING DATE: 06-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 21 571.7
FILING DATE: 06-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kitte, MONICAE C.
REGISTRATION NUMBER: 36,105
REGISTRATION NUMBER: 36,105
REGISTRATION NUMBER: 36,105
REGISTRATION NUMBER: 36,105
REGISTRATION NUMBER: 9564-3007
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                           STATE: D.C. COUNTRY: U.S.A. ZIP: 20005-5701
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 2, Application US/08258614
Patent No. 5432070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (202) 638-4810
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Best Local Similarity 66.7
Matches 6; Conservative
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97 RHKKPHNFS 105
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TOPOLOGY: linear
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US-09-252-991A-19828
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US-09-635-872A-15
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APPLICANT: Basilana, Frederic
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
APPLICANT: Deweille, Jan R.
TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
FILE REFERENCE: 989.6706P
CURRENT APPLICATION NUMBER: US/09/360,197
CURRENT FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
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66.7%; Pred. No. 93;
ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 2; Length 512;
Pred. No. 93;
1; Mismatches 2; Indels
                              COMPUTER KEALABLE FORM:

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,596
FILING DATE: US/08/828,596
FILING DATE: US/08/828,596
ATTORNEY/AGENT NUMBER: US/08/626,838
FILING DATE: US-ARR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mebel, Heidi S.
REGISTRATION NUMBER: Uirf n6-53
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEPHONE: 515-288-1338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-360-197-6; Sequence 6, Application US/09360197; Patent No. 6287859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.6%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 512 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 KHYKPKQFS 152
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KHFKPHGFS 9
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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RESULT 10

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Sequence 15, Application US/09635872A

Patent No. 6534300

GENERAL INFORMATION:
HILLIAM

TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOWAL HYDROLASES
FILE REFERENCE: 195613US0

CURRENT APPLICATION NUMBER: US/09/635,872A

CURRENT APPLICATION NUMBER: 60/153,831

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.0

SEQ ID NO 15

LENGTH: 908
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Facent No. 6551795
GENERAL INFORMATION:
APPLICANT: MART OF
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERCHGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
FRIOR PAPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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APPLICANT: CANFIELD, WILLIAM
TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
FILE REFERENCE: 199612050
CURRENT APPLICATION NUMBER: US/09/636,077A
CURRENT PILING DATE: 2000-08-10
PRIOR FILING DATE: 1999-09-14
PRIOR FILING DATE: 1999-09-14
NUMBER: OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 15
LENGTH: 908
TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-636-077A-15; Sequence 15, Application US/09636077A; Patent No. 6537785
                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 62.5%,
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 771 HRRPHGFA 778
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Matches 5; Conserv
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Sequence 6483, Application US/09328352
Batent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 4; Length 462
Pred. No. 1.3e+02;
0; Mismatches 1; Indels
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-6483
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Best Local Similarity 85.7%;
Matches 6; Conservative
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  374 HFKPH 378
                                                                RESULT 15
US-09-328-352-6483
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US-09-252-991A-25132
US-09-252-991A-25132

Sequence 25132, Application US/09252991A

Fatent No. 6551795

GENERAL INFORMATION:
MACTO TITLE OF INVENTION:
MACTO ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

FRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 363

LENGTH: 363
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                                                                                                                       Query Match 61.8%; Score 34; DB 4; Length 256; Best Local Similarity 71.4%; Pred. No. 67; Matches 5; Conservative 1; Mismatches 1; Indels
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APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT FILING DATE: 1999-07-02
EARLIER PEPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 20
LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/09347801; Patent No. 6262345; GENERAL INFORMATION:
                                       TYPE: PRT / OKGANISM: Pseudomonas aeruginosa US-09-252-991A-19828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25132
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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SEQ ID NO 19828
LENGTH: 256
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                                                                2003, 14:10:15; Search time 10.3333 Seconds (without alignments)
83.760 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                             283308 seqs, 96168682 residues
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Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
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T28848
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Gapop 10.0 , Gapext 0.5
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55
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Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
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Perfect score:
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T110404 T511044 T47978 G82590 G82594 T05797 T26701 149528 D95423 D95423 T22066 A45991 A90081	ALIGNWH nscription ision 06-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-	iption factor; Score 55; DB; Pred. No. 0.0
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J W W W W W W W W W W W W W W W W W W W	RESULT 1 A45377 Interaccription factor ATF4 N;Alternate names: activas C;Species: Homo sapiens (c) C;Accession: A45377; 1567; C;Accession: A45377; 1567; C;Accession: A45377; 1567; R;Karpinski, BA.; Morlo. U.; A;Itle: Molecular clonin, A;Reference number: A4537 A;Accession: A4537 A;Accession: A4537 A;Accession: A751 (KAR) A;Accession: A751 (KAR) A;Ttle: Molecular Clonin, A;Accession: 156787 A;Accession: 131 (KB) A;Accession: 134223 A;Accession	A;Map position C;Keywords; Di Query Match Best Local ( Matches ) Qy 1 Db 42 RESULT 2 S26812

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Gaps

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A;Molecule,type: DNA
A;Residues: 1.348 <TOM>
A;Cross-references: GB:AE000617; GB:AE000511; NID:g2314256; PIDN:AAD08150.1; PID:g231425
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; metalloprotein; oxidoreductase; zinc
C;Keywords: alcohol metabolism; dehydrogenase homology <LADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc-dependent alcohol dehydrogenase - Helicobacter pylori (strain J99)
C.Species: Helicobacter pylori
A;Variety: strain J99 |
B;Variety: Strain J99 |
B;Variety: Strain J99 |
C;Date: 12-Feb-1999 |
B;Variety: Strain J99 |
B;Variety: Strain J99 |
C;Date: 12-Feb-1999 |
C;Date: 12-Feb-1999
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A;Experimental source: strain J99
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A;Experimental source: strain VF5
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70485
A;Atatus: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-191 <AQF>
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Jun-1999
C;Accession: D70485
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C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase
F;27-335/Domain: long-chain alcohol dehydrogenase homology <LAD>
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C,Superfamily: protein kinase C inhibitor; histidine triad homology
F,45-150/Domain: histidine triad homology <HIT>
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78.2%; Score 43; DB 1; Length 348;
Best Local Similarity 87.5%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 1; Indels
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Pred. No. 2.5;
0; Mismatches 1; Indels
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Best Local Similarity 87.55,
7; Conservative
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Proc. Natl. Acad. Sci. U.S.A. 89, 5789-5793, 1992

Aritle: Protein interaction cloning in yeast: identification of mammalian proteins that A.Reference number: A46132; MUID:92335183; PMID:1631061

A.Recession: C46132

A.Ratus: nucleic acid sequence not shown; not compared with conceptual translation A.Rolecule type: mRNA

A.Residues: 246-381 < CHE1>
A.Residues: 246-381 < CHE1>
A.Residues: C46-381 < CHE1>
A.Residues: C46-381 < CHE1>
A.Residues: D.
A.Rolecule cextracted from NCBI backbone (NCBIP:108537)

A.Note: sequence extracted from NCBI backbone (NCBIP:108537)

Submitted to GenBank, November 1994
                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X61507; NID:g50049; PIDN:CAA43723.1; PID:g50050
R;Mielnicki, L.M.; Pruitt, S.C.
Nucleic Acids Res. 19, 6332, 1991
A;Title: Isolation and nucleotide sequence of a murine cDNA homologous to human activati
A;Reference number: S18719; MUID:92066493; PMID:1956797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A) Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: "MSFLNSEVLAGDLMS',51-381 CCHE2>
A; Residues: "MSFLNSEVLAGDLMS',51-381 CCHE2>
A; Cross-references: GB:M94087; NID:g293723; PIDN:AAA53043.1; PID:g567226
A; Experimental source: strain CD-1, embryo
A; Note: the submission of the complete sequence to GenBank is mentioned in reference A46
B; Vallejo, M.; Ron, D.; Miller, C.P.; Habener, J.F.
Proc. Natl. Acad. SCI. US.A. 9479-4683, 1993
A; Title: C/ATF, a member of the activating transcription factor family of DNA-binding pr
A; Reference number: A47443; MUID:93281642; PMID:8506317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - Helicobacter pylori (strain 26¢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: H64657
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S26812; S18719; Œ46132; A58861; A47443
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Kresidues: 'MTBNSTLNSEVLAGDLMS',51-376,'Q',378-381 <VAL>
A;Cross-references: GB:L1379!, NID:g293841; PIDN:AAA40476.1; PID:g293842
C;Keywords: transcription factor
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Pred. No. 0.22;
0; Mismatches
                                                                                                                            R.Pruitt, S.C. submitted to the EMBL Data Library, August 1991 A;Reference number: S26812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-57:59-288,'R',290-381 <MIE>
A;Cross-references: BML:X61507
R;Chevray, P.M.; Nathans, D.
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Best Local Similarity
                                                                                                                                                                                                                                                                      A, Accession: S26812
A, Molecule type: DNA
A, Residues: 1-381 <PRU>
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A; Reference number: 219086

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protein ClOC6.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Order (10-May-2001)
C;Accession: G88839
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Ganome sequence of the nematode C. elegans: a platform for investigating biologing A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ and www_sanger.ac.uk/Projects/ and www_sanger.ac.uk/Projects/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ and www_sanger.ac.uk/Projects/ and www_sanger.ac.uk
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R;Chapman, K.A.; Delauney, A.J.; Verma, D.P.S.
submitted to the EMBL Data Library, December 1992
A;Description: De novo purine biosynthesis in legume root nodules: cloning and sequencia A;Reference number: 845524
A;Accession: 845524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:chr_IV; PIDN:CAB05682.1; PID:g3874213; GSPDB:GN00022; CESP:C10C6
                                                                                                                                                                                                                                                                                                      A;Map position: 4
A;Introns: 40/2; 70/2; 101/3; 132/3; 176/1; 263/3; 310/2; 379/3; 427/1; 522/3; 587/3
C;Superfamily: fruit fly white protein; ATP-binding cassette homology
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Mar-1995
                                                                                                           A;Residues: 1-633 <WIL>
A;Residues: 1-633 <WIL>
A;Cross-references: EMBL:283217; PIDN:CAB05682.2; GSPDB:GN00022; CESP:C10C6.5
A;Experimental source: clone C10C6
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A;Accession: T19189
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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66.7%; Pred. No. 25;
7ative 2; Mismatches
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100.0%; Pred. No. 20;
tive 0; Mismatches
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Best Local Similarity 66./",
-hem 6; Conservative
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Best Local Similarity 66...
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457 KHFRIHGFA 465
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463 KHFRIHGFA 471
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A;Molecule type: DNA
A;Residues: 1-639 <STO>
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A;Molecule type: mRNA
A;Residues: 1-341 <CHA>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:L32150; NID:g476023; PID:g476024; PIDN:AAA29522.1
A;Cross-references: EMBL:L32150; NID:g476023; PID:g476024; PIDN:AAA29522.1
A;Cross-references: EMBL:L32150; NID:g476023; PID:g476024; PIDN:AAA29522.1
C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Ba
arbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phos
C;Keywords: ligase
F;96-2367/Domain: carbamoyl-phosphate synthase (ammonia) homology <CPA>
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C;Species: Yersinia pestis
C;Date: Oz.Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0095
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. Reparkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.Y.; Mhitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                          carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) II - malaria parasite C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T18410 R;Flores, M.V.C.; O'Sullivan, W.J.; Stewart, T.S. Submitted to the EMBL Data Library, March 1997 A;Description: Characterisation of the carbamoyl phosphate synthetase gene from Plasmodi A;Reference number: 218931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein YP00774 [imported] - Yersinia pestis (strain CO92)
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hypothetical protein C10C6.5 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 31-Jan-2000
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Pred. No. 15;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.9%;
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Best Local Similarity 77.5
Electron 7, Conservative
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                                                                                                           119 KEYKPHGFN 127
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173 HFSPYGFS 180
                                       1 KHFKPHGFS 9
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Best Local Similarity
6; Conserve
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A;Molecule type: DNA
A;Residues: 1-375 <KUR>
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R; White, S.
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21 FKPHGF 26

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FKPHGF 8

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Cipace: Arabidopsis thaliana (mouse-ear cress)
Cipace: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cipacession: A96560
A)Authors: Hunter, Julyar, L.
A)Authors: Hunter, Julyar, L.
Cipacession: A1, Julyar, L.
A)Authors: Hunter, Julyar, L.
A)Authors: Hunter, Julyar, L.
A)Authors: Salzberg, L.; Schwartz, Julyar, E.; Kim, C.
Cipacession: A1, L.; Changer, L.; Schwartz, Julyar, E.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Altle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A)Accession: A96560
A)Accession: A96560
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                             A;Reaidues: 1-411 <WIL>
A;Cross-references: EMBL:Z81015; PIDN:CAB02660.1; GSPDB:GN00028; CESP:C11E4.3
A;Experimental source: clone C11E4
                        Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
Cipacession: T19195
Simbartimore, B.
Submitted to the EMBL Data Library, October 1996
A;Reference number: Z19087
A;Accession: T19195
A;Accession: T19195
A;Accession: T19195
A;Accession: T19195
A;Accession: DNA
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R;Nhan, M; Le, T.T.  
submitted to the EMBL Data Library, April 1996  
A;Description: The sequence of C. elegans cosmid F19G12.
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hypothetical protein C11E4.3 - Caenorhabditis elegans
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Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: CESP:C11E4.3
A;Map position: X
A;Introns: 12/3; 91/3; 136/2; 182/3; 230/3; 307/3
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Best Local Similarity 75.vv.,
6; Conservative
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A; Botecule type: protein
B; Sletten, K.; Husebekk, A.; Husby, G.
S; Sletten, K.; Husebekk, A.; Husby, G.
S; Sletten, K.; Husebekk, A.; Husby, G.
A; Accession: A28573; MUID:87291864; PMID:3616485
A; A28573; MUID:87291864; PMID:3616485
A; A28573; MUID:87291864; PMID:3616485
A; A28573; MUID:87291864; PMID:3616485
A; A28574864; PMID:36164864; PMID:36164864; PMID:36164864; PMID:36164864; PMID:3616486
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A,Cross-references: BMBL:U58756, PIDN:AAC48087.1; GSPDB:GN00022; CESP:F58F9.1
A,Experimental source: strain Bristol N2; clone F58F9
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Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispate: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 29-0ct-1999
Cispate: 29-0ct-1999
Rivelson, J.; Wohldmann, P.
Submitted to the EMBL Data Library, May 1996
A; Description: The sequence of C. elegans cosmid F58F9.
A; Reference number: 220531
A; Reference number: 220531
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from CB/EMBL/DDBJ
                                                                                                                                                                                                                         Serum amyloid A protein - horse
N;Contains: amyloid protein AA
C;Species: Equus caballus (domestic horse)
C;Date: 19-Nov-1988 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
C;Accesion: A60430, A28573
R;Sletten, K.; Husebekk, A.; Husby, G.
Scand. J. Immunol. 30, 117-122, 1989
A;Title: The primary structure of equine serum amyloid a (SAA) protein.
A;Reference number: A60430; MUID:89332320; PMID:2502829
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Pred. No. 9.7; 1; Mismatches

83.3%;

Query Match 67.3° Best Local Similarity 83.3° Matches 5; Conservative

||:||| 100 HFRPHG 105

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2 HFKPHG 7

hypothetical protein F58F9.1 - Caenorhabditis elegans

179 NFKPHGIS 186

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2 HFKPHGFS

Query Match Best Local Similarity Matches 6; Conserv

A, Gene: CESP: F58F9.1 A; Map position: 4

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A;Accession: T29884
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Wolecule type: DNA
A;Wolecule type: DNA
A;Wolecule type: DNA
A;Cossidues: 1-668_<nNA>
A;Cross-references: EMBL:U51997; PIDN:AAC48156.1; GSPDB:GN00028; CESP:F19G12.2
A;Experimental source: strain Bristol N2; clone F19G12
A;Genetics:
A;Gene: CESP:F19G12.2
A;Map position: X
A;Introns: 444/3; 561/2
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Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 1; Indels
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314 NFKPHGIS 321
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Search completed: December 16, 2003, 14:19:19 Job time : 11.3333 secs

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Q9ES19
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Q81cf69 mus musculu
Q61328 mus musculu
Q61328 mus musculu
Q25732 helicobacte
Q9782 qquifex aeo
Q95y12 aquifex aeo
Q95y132 plasmodium
Q27732 plasmodium
Q87773 plasmodium
Q87773 plasmodium
Q87773 gossypium s
Q86016 methanosarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  092p43 rhizobium m
08vzw9 vigna ungui
09vpw4 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9es19 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                          December 16, 2003, 14:09:45; Search time 25 Seconds (without alignments) 92.899 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Q8CF69
Q8CF69
Q25732
Q9ZKA9
Q9ZKA9
Q8TBN3
Q81EN3
Q8ZHV7
Q9SMF3
Q8QD16
Q9ZWY9
Q9ZWY9
Q9ZWY9
Q9ZWY9
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p_vertebrate:*
p_unclassified:*
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sparcha:*
spaceria:*
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sphuman:*
spinvertebrate:*
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_bacteriap:*
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seq length: 200000000
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sp_rodent:*
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55
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Match Length
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Perfect score:
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Maximum DB 8
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Opnoy equus cabal
Oppos xanthomonas
Opos xanthomonas
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Q9lif1 lymantria d
Q9lim2 arabidopsis
Q933e7 helicobacte
Q98tp6 platichthys
Q9K9n9 bacillus ha
O34743 bacillus su
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Nehring R.B:, Horikawa H.P.M., El Far O., Kneussel M.,
Brandstatter J.H., Stamm S., Wischmeyer E., Betz H., Karschin A.;
"The Metabotropic GARAB Receptor Directly Interacts with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00339; BRLZ; 1.
PROSTIE; PS00054; BZIE BASIC; 1.
DNA-binding; Nuclear procein.
SRQUENCE 347 AA; 38151 MW; CCEGED02F263296B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Activating Transcription Factor 4.";
J. Biol. Chem. 275:35185-35191 (2000).
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY.
EMBL, AFS25627, AAG31732.1;
InterPro; IPR004827; TF bZIP.
Pfam; PF00170; bZIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Activating transcription factor ATF-4 Rattus norvegicus (Rat).
            Q8P5G5
Q9D7Q0
Q9CL80
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Q9N882
Q9VC48
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Q9K9N9
Q34743
                                                                                          023831
Q9SSV0
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Q8E8N8
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Q98MP8
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091/IM2
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                                                                 Q90613
Q93205
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  PRELIMINARY;
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Best Local Similarity
9; Conserv
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Q96AQ3

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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Activating TRANSCRIPTION factor 4 (Activating TRANSCRIPTIONN factor 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S., Loftus B., Richardson D., Dodgon R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gooayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 119-381 FROM N.A.
MEDLINE=92183900; PubMed=1371974;
Nishizawa M., Nagata S.;
"CDNA clones encoding leucine-zipper proteins which interact with G-CSF gene promoter element 1-binding protein.";
FEBS Lett. 299:36-38(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H71104.
H21104.
H211cobacter pylori (Campylobacter pylori).
H21icobacteraceae; Felicobacter.
H21icobacteraceae; H21icobacter.
NCBI_TAXID=210;
                                                                                                                                                                                             SEQUENCE FROM N.A.

SEALAL=129/SV;

MEDLINE=22066433; PubMed=1956797;

Mielnicki L.M., Pruitt S.C.;

Mielnicki L.M. orucleotide sequence of a murine cDNA homologous to human activating transcription factor 4.";

Nucleic Acids Res. 19:6332-6332(1991).
                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49; DB 11; Length 381;
Pred. No. 0.5;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                      Nishizawa M., Nagata S.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD: MGI: 80056; ALF4.
InterPro; IPR004827; TF_bZIP.
PFam; PF00170; bZIP; 1.
SMART; SM00338; BRLZ; 1.
PROSITE; PS00036; BZIP_BASIC; 1.
DNA-binding; Nuclear protein.
SEQUENCE 381 AA; 41810 MW; 9FC3A0CA16EB7431 CRC64;
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Last sequence update)
Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Cinnamyl-alcohol dehydrogename EL13-2 (CAD)
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EMBL; X61507; CAA43723.1; -.
EMBL; AB012277; BAA25314.1; -.
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STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 119-381 FROM N.A.
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Best Local Similarity 88.7°,
8; Conservative
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74 KHLKPHGFS 82
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                                                                                                                                                           NCBI_TaxID=10090;
                                                                                 ATF4 OR ATF-4.
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium.
The RANTOM Consortium.
The RANTOM Consortium Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AKO03001; BAC25014.1; -.
SEQUENCE 350 AA; 38715 MW; 6394500297E6C3CE CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 55; DB 4; Length 351; 100.0%; Pred. No. 0.035; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.1%; Score 49; DB 11; Length 350; 88.9%; Pred. No. 0.46;
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                                                                                                                                                                                                                                                    SMART; SM00338; BRLZ; 1.
PROSITE; PS00036; BITE BASIC; 1.
Hypothetical protein; DNA-binding; Nuclear protein.
SEQUENCE 351 AA; 38589 MW; 3BBB7379DC3B0D07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.1-MAR-2003 (TrEMBLrel. 23, Created)
0.1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
0.1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Activating transcription factor 4.
                                                                                     Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Created)
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                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004827; TF bZIP.
Pfam; PF00170; bZIP; 1.
                                                                 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
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Matches 9; Conservative
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                               PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Q8CF69

RESULT 3

961328

RESULT 4 Q61328 ID Q6133 AC Q6133 DT 01-NC

Matches

Query Match

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Gaps

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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Carbamoyl phosphate synthetase II (EC 1.4.3.6) (Copper amine oxidase)
(Fragment).
                                                                                                                                                                                                                                                   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Shead M.A., Keller M., Aulay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; Inthe complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Katrib M.T., Stewart T.S.;
"Carbamoyl phosphate synthetase II gene from Plasmodium vivax.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) = RCHO + NH(3)
-!- COFACTOR: BINDS 1 COPPER ION AND 1 TOPAQUINONE PER SUBUNIT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
-!- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.
EMBL; AF327646; AAK15525.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
NCBI_TaxID=5855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.5%; Score 41; DB 16; Length 191; 66.7%; Pred. No. 7.6; ive 2; Mismatches 1; Indels
                                                                                                                              Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
101-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein AQ_2159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00098; CPSASE.
PROSITE; P801164; COPPER AMINE_OXID_1; 1.
PROSITE; P800867; CPSASE_2; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
Copper; Oxidoreductase; TPQ.
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InterPro; IPR005483; CPase L.
InterPro; IPR005480; CPase L. D2.
InterPro; IPR005480; CPase L. D3.
InterPro; IPR005580; CPase L. D3.
InterPro; IPR000531; TonB boxC.
Pfam; PF02786; CPase L. D2; 1.
Pfam; PF02787; CPase L. D2; 1.
                                                                                                                                                                                                                    STRAIN=VF5;
MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                               Nature 392:353-358(1998).
EMBL; AE000776; AAC07886.1; -.
InterPro; IPR001310; HIT.
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Best Local Similarity 66....
6; Conservative
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                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium vivax.
                                                                                                                  Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                   aeolicus.
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                                                               Nature 388:539-547 (1997).
-!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
-PAMILY.
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gastric pathogen Helicobacter pylori.";
Nature 397.716.180(1999).
-!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99120557; PubMed=9923682; Alm R.A., Ling L.S.L., Brown B.D., Doig P.C., Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G. Turmino P.J., Caruso A. Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria: Proteobacteria: Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic sequence comparison of two unrelated isolates of the human
                                  "The complete genome sequence of the gastric pathogen Helicobacter pylori.";
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                                                                                                                                                   EMBL, AEGOGOLT, AADO8150.1; -.
TIGR, HP1104; -.
InterPro; IPRO22328; ADH_zinc.
InterPro; IPRO2085; Adh_zn_family.
PROSITE; PSO0059; ADH_ZINC; 1.
Hypothetical protein; Oxidoreductase; Zinc; Complete proteome.
SEQUENCE 348 AA; 38645 MW; 07D7E1A63048EF48 CRC64;
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                           78 2%; Score 43; DB 16; Length 348; 87.5%; Pred. No. 5.9; artive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.2%; Score 43; DB 16; Length 350; 87.5%; Pred, No. 5.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001531; AAD06610.1; -.
InterPro; IRR0020328; ADH zinc.
InterPro; IRR002085; Adh zn_family.
Pfam; PF00107; adh zinc; -1.
PROSITE; PS00059; ADH ZINC; 1.
Oxidoreductass; Zinc; Complete proteome.
SEQUENCE 350 AA; 38939 MW; OCC26211002E6CD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Zinc-dependent alcohol dehydrogenase.
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Matches 7; Conservative
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SEQUENCE FROM N.A.
                        Venter J.C.;
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InterPro; IPR002048; EF-hand.
                                                                          InterPro; IPR006275; CarA_L_glu.
InterPro; IPR006274; CarA_small.
EMBL; L32150; AAA29522.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.00.,
Rest Local 7; Conservative
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SEQUENCE FROM N.A.
Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
Barriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL844509; CAD52216.1;
                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H(2)O(2).
-!- COFACTOR: BINDS 1 COPPER ION AND 1 TOPAQUINONE PER SUBUNIT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) = RCHO + NH(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=FCQ27; Plores M.V.C., O'Sullivan W.J., Stewart T.S.; "Characterisation of the Carbamoyl Phosphate Synthetase Gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Carbamoyl phosphate synthetase II (BC 6.3.5.5) (Copper amine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF13_0044.
Plasmodium falciparum (isolate 3D7).

Eukaryota, Alveolata, Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=36329;
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                                                                              Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                        Indels
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   36844 MW; 6C5001566CDC5E8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Carbamoyl phosphate synthetase, putative (EC 6.3.5.5)
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                                                                      74.5%; Score 41; DB 77.8%; Pred. No. 13; tive 1; Mismatches
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Best Local Similarity 77...
7; Conservative
                                                                                                                                                            Conservative
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1154 KYFKKHGFS 1162
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           321 AA;
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les 7; Conserv
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SEQUENCE
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           SEQUENCE
                                                                                     Query Match
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Q27732;
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Q8IEN3;
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1732 1732 1732 1733 1733 1734

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STRAIN=KIM5 / Biovar Mediaevalis;
MEDILNB=22137865; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CO-92 / Biovar Orientalis;

MEDLINB=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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PROSITE; PS01164; COPPER_AMINE_OXID_1; 1.
PROSITE; PS00867; CPSASE_1; 1.
PROSITE; PS00087; CPSASE_2; 2.
PROSITE; PS00018; EF HAMD; 1.
COpper: Ligase; Oxidoreductase; TPO.
SEQUENCE_2391 AA; 275674 MW; 426F3C3E612FEEE2 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein YP00774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 AA
                                                                                                                                                                                                                                                                                                InterPro; IRR00191; GATase 1.
InterPro; IPR00191; GATase 1.
InterPro; IPR00191; GATase 1.
InterPro; IPR00191; GATase 1.
Pfam; PF00189; CPSase 1.
Pfam; PF00189; CPSase 1.
Pfam; PF00189; CPSase 1.
Pfam; PF00117; GATase; 1.
Pfam; PF00117; GATase; 1.
Pfam; PF00199; CPSASE.
PRINTS; PR00099; CPSASE.
PRINTS; PR00099; CPSATASE.
PRINTS; PR00099; CRSGATASE.
TIGRPAMS; TIGR01369; CPSASEIISmall; 1.
TIGRPAMS; TIGR01369; CPSASEIISmall; 1.
TIGRPAMS; TIGR01369; CPSASEIISMAP ONTH.
InterPro; IPR005483; CTase_L.
InterPro; IPR005479; CPase_L.D2.
InterPro; IPR005480; CPase_L.D3.
InterPro; IPR005481; CPase_L.D.
InterPro; IPR005494; CPase_E.M.
InterPro; IPR001317; CPS_GATase.
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Gaps

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RESULT 12

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Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C., Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S., Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P., Fritz H.-J., Gottschalk G., "The genome of Methanosarcina mazei: evidence for lateral gene transfer between Bacreria and Archaea "; J. Mol. Microbiol. Biotechnol. 4:453-461(2002). BRBL, AB012254, AAM29846.1; -Complete proteome: Hypotherical protein. SEQUENCE 289 AA; 32222 MW, AF59E9997E30ADF6 CRC64;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S., Godrien T., Goffeau A., Rahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont
                                                                                                                                                                                                                                                                                  Score 38; DB 17; Length 289;
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RÕI950 OR SMCÕ4290.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
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01-MAR-2002 (TrEWBLrel. 20, Last sequence update)
01-0GT-2002 (TrEWBLrel. 22, Last annotation update)
Succinoaminoimidazolecarboximide ribonucleotide synthetase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 19, Last sequence update) Hypothetical protein R01950.
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Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001)
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MEDLINE=21396507; PubMed=11481430;
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EMBL; ALS1789; CAC46529.1; -
InterPro; IPROQU3304; FMCA, AmdA.
Pfam; PF03069; FMCA, AmdA, All
Hypothetical protein; Complete p
                                                                                                                                                                                                                                                                                           69.18;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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Best Local Similarity
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Q92P43
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Brubaker C.L., Liu Q., Green A.G., Marshall D.R., Singh S.P.;

Brubaker C.L., Liu Q., Green A.G., Marshall D.R., Singh S.P.;

"Microsomal omegaé desaturase intron topologies contribute to our
understanding of reticulate evolution in Gossypium (Malvaceae) and the
evolution of the Australian Gossypium species.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ244917; CAB5280.1; -.
NON TER
     Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gossypium stocksii.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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                                                                                                                                                                                                                                                          Score 39; DB 16; Length 375;
Pred. No. 35;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 10; Length 51;
Pred. No. 7.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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Methanosarcinaceae, Methanosarcina.
                                                                        "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).

EMBL; AJ41444; CAC89623.1; --
EMBL; ABC103944; AAM86968.1; --
Hypothetical protein; Complete proteome.

SEQUENCE 375 AA; 41623 MW; AAIF781311AC9ABO CRC64;
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STRAIN=Goe1 / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
MEDLINE=22120827; PubMed=12125824;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Microsomal omega6 desaturase enzyme (Fragment).
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Last sequence update)
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                                                                                                                                                                                                                                                             70.9%;
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75.0%;
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5728 MW;
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                                                                                                                                                                                                                                                       Query Match 70.9
Best Local Similarity 75.0
Matches 6; Conservative
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KPFRPHGF 46
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                                                   Perry R.D.;
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1D Q9SMF3
1D Q9SMF3
DT 01-MAY:
DT 01-MAY:
DE Microsol
GN Gossypi:
GN Gossypi:
CC Spermat

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Matches

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OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.

NOBI TaxID=3917;

RP SEQUENCE FROM N.A.

RC STRAIN=CV. Vita 3.

RA Smith P.M.C., Mann A.J., Reck V.;

Smith P.M.C., Mann A.J., Reck V.;

RT Tibonucleotide synthetase.";

RI Submitted (NOV-2001) to the EWBL/GenBank/DDBJ databases.

C. I-CATALYTIC ACTIVITY: ATP + 5-AMINO-1-(5-PHOSPHO-E ADP + PHOSPHATE + CATALYTIC ACTIVITY: ATP + 5-AMINO-1-(5-PHOSPHO-E ADP + PHOSPHATE + CATALYTIC ACTIVITY: ATP + 5-AMINO-1-(5-PHOSPHO-E ADP + PHOSPHATE + CATALYTIC ACTIVITY: ATP + 5-AMINO-1-(5-PHOSPHO-E) REBOSYL) IMIDAZOLE-4-CARBOXAMIDO] SUCCINATE:

C. I- PATHWAY: DE NOVO PURINE BIOSYNTHESIS; SEVENTH STEP.

C. I- STMILARITY: BELONGS TO THE SAICAR SYNTHETASE FAMILY.

C. I- STMILARITY: BELONGS TO THE SAICAR SYNTHETASE FAMILY.

DR PRODON; PRO003643; SAICAR SYNT.

DR PRODON; PRO01636; SAICAR SYNTHETASE 1; 1.

DR PROSITE; PS01059; SAICAR SYNTHETASE 2; 1.

R Ligase; Purine biosynthesis.

SQ SEQUENCE 402 AA; 45054 WW; 23FCB2DC29BAE3BD CRC64;

Query Match

Ouery Match

Best Local Similarity 100.0%; Pred. NO. 57;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: December 16, 2003, 14:18:04 Job time: 26 secs

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S. epidermidis operhuman angiopoietin Human angiopoietin Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Human polypeptide M. tuberculosis an Mycobacterium tuber tuberculosis an Mycobacterium tuberculosis and Mycobacterium tuberculosis CDT. gondii immunoge Mouse ageing inhib Streptococcus pneu Etreptococcus pneu Human protein agedu Novel human diagno Herbicidally activ Streptococcus pneu Glutamyl tRNA synt
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Prophenol oxidase.
Staphylococcus epi
Mouse ageing inhib
Human novel foetal
                                                                        Listeria monocytog
Drosophila melanog
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                                           Drosophila melanog
Drosophila melanog
            colon cancer
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                                         ABB66825
ABB69124
ABB49129
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AAG44592
AAG61759
AAO02856
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AAB95039
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AAG82101
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 30-MAY-2001; 2001WO-US17454.
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20-DEC-2000; 2000US-257007P
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Synthetic.
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 Human cancer antig
Drosophila melanog
Bombyx mori (pro)p
Human G protein-co
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Human cancer antig
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(c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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AAU25704
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Gapop 10.0 , Gapext 0.5
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been raised in vitro or in vivo in the presence and at the expense of an antigen presenting cell that presents the immunogenic compound in the control of adoptive immunotherapy comprising administering the immune the effector cell. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are especially useful in gene therapy or as components of anti-cancer vaccines. The compounds are useful for treating cancer, particularly covarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These antibodies are further useful for immunotherapy when administered to a subject. The peptides polypeptides and polymolectides are useful in diagnostic methods, for the detection and purification of antibodies, or as immunogens for the production of antibodies. The present
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                                                                                                                The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATF4/CREB-2 (not defined) and the polynucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune responses in a subject by delivering the compound, a method of immunotherapy comprising administering to a subject the antibody, an immune effector cell that has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respectivel but have not been cross-referenced or CDS features put in due to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
      useful for
New therapeutic compounds comprising immunogenic ligands, useful modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB61794 standard; Protein; 690 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        degeneracy of the DNA sequences.
                                                                                Claim 1; Page 55; 68pp; English.
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity
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                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher uevaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cancer antigen; ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATF4/CREB-2 (not defined) and the polynucleotides encoding them.
                                                                                                                                                                                                                                                                   (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                  Disclosure; SEQ ID NO 12174; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer antigen ATF4/CREB-2 based immunogenic ligand #4.
                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 22; Length 690;
Pred. No. 39;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU74684 standard; Peptide; 9 AA.
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Similarity 71.4%;
5; Conservative
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20-DEC-2000; 2000US-257007P.
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WPI; 2001-656860/75.
N-PSDB; ABL05897.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          690 AA;
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                                                                                      interactions -
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The B. mori silkworm larvae derived (pro)phenoloxidases Phe52-Val693 (AAR89114) and Phe52-Cly685 (AAR89115), are encoded by AAT10240 and AAT10241, respectively. The (pro)phenoloxidases can be used as new labelling oxidases.
                                                                               insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Pro)phenol:oxidase from silkworm - useful as a labelling oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Silkworm; larvae; pro; phenoloxidase; Phe52-Val693; Phe52-Gly685
                                                                                                                                                                                                                                                                                      Length 683;
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                                                                                                                                                                                                                                                               Score 40; DB 22; Length be. Pred. No. 1.2e+02;
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Pred. No. 1.3e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bombyx mori (pro)phenoloxidase Phe52-Val693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "peptide fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR89114 standard; Protein; 693 AA
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52..61
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Best Local Similarity
These 5; Conserve
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                                                                                                                                              (ABB57737-ABB72072).
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                                                                                                                                                                                                                                              683 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            labelling oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT10240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-1996
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                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR89114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
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                                                      administering to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antigen presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune effector cell. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are especially useful in gene therapy or as components of anti-cancer vaccines. The compounds are useful for treating cancer, particularly ovarian cancer. The compounds are also useful for generating antibodies antibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polymucherapy when administered to a subject. The peptides, polypeptides and polymucherapy when administered to a subject. The peptides, polypeptides and polymucherapy when administered to a subject. The peptides are useful in a special in a subject the peptides, polypeptides and polymucherapy when administered to a subject. The peptides are useful in a special in a subject the peptides of the subject the subje
  Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising
                                                                                                                                                                                                                                                                                                                      diagnostic methods, for the detection and purification of antibodies, or as immunogens for the production of antibodies. The present sequence represents a human cancer antigen ATF4/CREB-2 based immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                            respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respect but have not been cross-referenced or CDS features put in due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 23; Length >;
Pred. No. 9.3e+05;
Triantches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degeneracy of the DNA sequences.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                     igand of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
N-PSDB; ABL03607.
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es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FLYKWHGFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Gaps

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Phe52-Val693

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G protein-coupled receptors termed nGPCR-x. nGPCR-x polynucleotides, and modulators may be used in the treatment of diseases and conditions such as infections, such as vival infections caused by HIV-1 (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, annorexia, hypotension, hypertension, myocardial infarction, atherosclerosis), Parkinson's disease, and psychotic and neurological disorders, including schizophrenia, migraine, major depression, anxiety, mental disorder, manic depression, and dyskinesias, such as Huntington's disease or Tourette's Syndrome and many other diseases and syndromes listed in the specification. nGPCR-x polynucleotides and polypeptides, as well as nGPCR-x modulators, may also be used in diagnostic assays for such diseases or conditions. The present sequence represents a G protein-coupled receptor
                                                                                                                                                                                                                                                                                                 minging processing the copies of the control of the cardiant; antidabetic; moretic; hypotensiue; hypotensiue; antidatic; cardiant; antidabetic; ancretic; hypotensiue; hypotensiue; antiparkinsonian; nootropic; neuroprotective; antidepressant; viral infection; HIV-1; human immundeficiency virus; HIV-2; pain; cancer; metabolic disease; cardiovascular disease; type 2 diabetes; obesity; anorexia; hypotension; hypertension; myocardial infarction; atheroscierosis; parkinson's disease; psychosis; neurological disorder; schizophrenia; migraine; major depression; atisease; rourette's Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel isolated nucleic acid molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecules encoding G protein-coupled receptors cermed nGPCR-x, useful in the treatment and diagnosis of viral infections, cancers and mental disorders (e.g. Parkinson's disease and
                                                                                                                                                                                                                                                                                      Human; G protein-coupled receptor; nGPCR-x; antiviral; analgesic;
                                                                                                                                                                                                                                           Human G protein-coupled receptor nGPCR-2289.
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                                                                                                                       AAU19356 standard; Protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2000; 2000US-0187583.

08-MAR-2000; 2000US-0187584.

08-MAR-2000; 2000US-0187639.

08-MAR-2000; 2000US-0187639.

08-MAR-2000; 2000US-0187707.

08-MAR-2000; 2000US-0187707.

08-MAR-2000; 2000US-0187708.

08-MAR-2000; 2000US-0187709.

08-MAR-2000; 2000US-0187709.
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401 FFYRWHAYI 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                     04-DEC-2001
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                                                                                                                                                               AAU19356;
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                                                                                                                                                                                                                                                                                                                                                                   Human; mental disorder; thyroid disease; renal failure; anorexia; inflammatory condition; Crohn's disease; rheumatoid arthritis; HIV; autoimmune disorder; schizophrenia; migraine; stroke; dementia; obesity; depression; Parkinson's disease; Alzheimer's disease; viral infection; thuthington's disease; human immunodeficiency virus; type 2 diabetes; anorexia; hypotension; hypetension; thrombosis; myocardial infarction; atherosclerosis; cancer; sexual dysfunction; G protein-coupled receptor;
                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for use in the treatment of mental disorders, such as Alzheimer's disease, or Parkinson's disease -
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                                            66.7%; Score 38; DB 22; Length 184; 44.4%; Pred. No. 73;
                                                                             2; Indels
                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lind P;
                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor, nGPCR-2118.
                                                                                                                                                                                                                                    AAU25704 standard; Protein; 220 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parodi LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FBB-2000; 2000US-0184602.
24-FBB-2000; 2000US-0184604.
24-FBB-2000; 2000US-0184606.
24-FBB-2000; 2000US-0184699.
24-FBB-2000; 2000US-0184110.
24-FBB-2000; 2000US-0184112.
24-FBB-2000; 2000US-0184115.
24-FBB-2000; 2000US-0184115.
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                                                                                                                                                                                                                                                                                                     (first entry)
                                                                               4; Conservative
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119 YFYRWHTFI 127
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                                            Query Match
Best Local Similarity
                                                                                                               1 FLYKWHGFV
              184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domo sapiens.
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               Sequence
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Human, cancer antigen; ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.

30-MAY-2001; 2001WO-US17454.

WO200192306-A2.

06-DEC-2001

sapiens

Synthetic.

31-MAY-2000; 2000US-209388P. 20-DEC-2000; 2000US-257007P.

(GENZ ) GENZYME CORP.

WPI; 2002-097764/13.

Nicolette CA;

Human cancer antigen ATF4/CREB-2 based immunogenic ligand #3.

(first entry)

09-APR-2002

AAU74683;

AAU74683 standard; Peptide; 9 AA.

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atherosclerosis, cancer, and sexual dysfunction. AAU25617-AAU25726 represent the amino acid sequences of novel human G protein-coupled receptors, nGPCR-2031 to nGPCR-2140 respectively, as described in the
                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 87;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                       6; Conservative
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                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                              220 AA;
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                                                                                                       invention
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                                                                                                                                                                                 Sequence
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ID ABB 3

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New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines

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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer cantigon ATF4(FRB-2 (not defined) and the polynucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising candinistering to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an entigen presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response context coll. The compounds are useful for modulating an immune response of the synthetic and naturally occurring compounds. The compounds are useful for treating cancer, particularly covarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These compounds context of antibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polynicleotides are useful in diagnostic methods, for the detection and purification of antibodies. The sequence represents a human cancer antigen ATF4(CRB-2 based immunogenic interview) is an antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AA220120-AAS20125 respectively but have not been cross-referenced or CDS features put in due to the degeneracy of the DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 23; Length 9;
Pred. No. 9.3e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 55; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ligand of the invention.
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Best Local Similarity
Matches 6; Conserv
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Gaps

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Score 38; DB 23; Length 448; Pred. No. 1.8e+02; 0; Mismatches 2; Indels

66.7%; 75.0%;

Query Match Best Local Similarity

448 AA;

Seguence

Conservative

. 9

Matches

α

FLYKWHGF

н æ

FLYPWFGF 15

σ RESULT Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 17.

(HUMA-) HUMAN GENOME SCI INC

99US-0157137. 99US-0163280.

29-SEP-1999; 03-NOV-1999;

28-SEP-2000; 2000WO-US26524

WO200122920-A2 Ношо варіепв.

05-APR-2001.

Human colon cancer antigen protein SEQ ID NO:5210.

(first entry)

03-SEP-2001

AAG74446 standard; Protein; 92 AA.

AAG74446

1 FLHKWHWVV 9

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can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTS) for human secreted proteins expressed in prostate, and encode the proteins given in AAV171916 to AAV11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used for producing secreted human gene therapy. The proteins obtained may have cytokine activity, cell prollferation and differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activity, anti-inflammatory
                                                                                                                                                                                             forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  directing extracellular secretion of a polypeptide or the insertion polypeptide into a membrane, or importing a polypeptide into a cell
                                                                                                                                                                        Human; secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.9%; Score 37; DB 20; Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lacroix B;
                                                                                                                                   Human 5' EST secreted protein SEQ ID No: 530,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 34; Page 636; 675pp; English.
                  AAY11930 standard; Protein; 23 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-IB01232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0905144.
                                                                                            18-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-153780/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX40652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET.
                                                                                                                                                                                                                                                                                                                                                   WO9906550-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1997;
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            11-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duclert A,
                                                       AAY11930;
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens. The colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene the reatment of diseases associated with inappropriate postersion. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. The inactive proteins. N and P can be used in the prevention, diagnosis and AAB77789 represent of colorectal carcinomas and cancers. AAH37196 to AAH37204
                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosing and/or treating colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 6892-6893; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB11269 standard; peptide; 151 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for preventing,
                                                                                                                                                                                                                                                                                                                                                             Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||| |
6 LFKWHNF 12
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Indels

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Pred. No. 13; 1; Mismatches

66.7%;

Conservative

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RESULT 11

1 FLYKWHGFV 9

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03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                            05-FEB-2001; 2001WO-US03800.
                                                                                                e.g. arthritis and cancer
                                                                                   WPI; 2001-457740/49.
                                                                         (HYSE-) HYSEQ INC.
                                                                                      N-PSDB; ABA08513
                                                 WO200157188-A2
                                            Homo sapiens.
                                                      09-AUG-2001
                                                                              rang YT,
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Myers EW; ABB66825 standard; Protein; 517 AA. Li PWD, 23-MAR-2001; 2001WO-US09231. 23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150. (first entry) Local Similarity 66.7 les 6; Conservative Drosophila melanogaster. 5; Conservative 35 FLYVWGGYV 43 Q Venter JC, Adams M, WPI; 2001-656860/75. 1 FLYKWHGFV sequences (ABL01840 (ABB57737-ABB72072) (PEKE ) PE CORP NY. Query Match Best Local Similarity 517 AA; N-PSDB; ABL10928 151 pharmaceutical WO200171042-A2 interactions -26-MAR-2002 27-SEP-2001, Sequence ABB66825; Query Match Sequence Matches Matches ABB66825 88888888 à 셤 Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, and the control of the invention, and methods of detecting the nucleotides, antibodies against the polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention have homology to known proteins, thereby cylopeptides of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby cylopeptides of the invention have homology to known proteins, thereby cylopertial therapeutic applications. The polypeptides of the invention activities, including cytokine, cell proliferation or cell afferentiation activities, stem cell growth factor activity; immunomodulatory activity; tissue growth activity; immunomodulatory activity; activities, theomotic or chemokinetic activities, hambin-related activities, chemocatic or chemokinetic activities, hambin-related activities, chemocatic or chemokinetic activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions includes cande encoding them) may be used to promoce wound repair (or nucleic acide encoding them) may be used to promoce wound repair (or nucleic acide encoding them) may be used to promoce wound repairs and fungal infections and ulcers), while those with activity may be used in the treatment of viral, bacterial and fungal infections and ulcers), while the seq to promote cell growth. For example, such polypeptides may be used to neurcopithelial collustry. Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoissis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiniflammatory; antiathmatic; antiathritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer. Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject Human LCP homologue, SEQ ID NO:1639 Claim 20; Page 161; 1963pp; English. Liu C, Drmanac RT;

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that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 egecification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                    22; Length 151;
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                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 27267.
                                                                                                                                                                                                                                                                                            64.9%; Score 37; DB 66.7%; Pred. No. 89; tive 1; Mismatches
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3 YKWHG 7

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Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.

Listeria monocytogenes.

WO200177335-A2. 18-OCT-2001 11-APR-2001; 2001WO-FR01118. 11-APR-2000; 2000FR-0004629.

(INSP ) INST PASTEUR

Dehoux P; Cossart P;

Amend A; Durant L;

Buchrieser C, Frangeul L, Couve B, Rusniok C, Fsihi H, Dehoux P Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA, Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L, Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J,

treatment

Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections,

Claim 6; SEQ ID No 1834; 192pp; French.

related polypeptides

WPI; 2002-010914/01.

Voss H;

Rose M,

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.w1po.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 34164; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.9%; Score 37; DB 22; Length 524; 100.0%; Pred. No. 3.1e+02;
                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 34164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Prec. ...
                                                                                                                                                                                                                                                                                   Myers
                                                    ABB69124 standard; Protein; 524 AA.
                                                                                                                                                                                                                                                                                  PWD,
                                                                                                                                                                                                                23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                          26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                 Ľ
                                                                                                                                                        Drosophila melanogaster
                                                                                                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75.
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       509
                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                             N-PSDB; ABL13227
     505 YKWHG
                                                                                                                                                                            WO200171042-A2
                                                                                                                                       pharmaceutical
                                                                                                                                                                                              27-SEP-2001
                                                                                                                                                                                                                                                                                Venter JC,
                                                                       ABB69124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
                                 RESULT 14
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The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
it are useful for selecting probes and primers for detecting genes in L.

compocytogenes and related organisms, and for studying genes in L.

monocytogenes and related organisms, and for studying genes in L.

compocytogenes and related organisms, and for studying genetic

composition the genome sequence are useful for rataing specific

antibodies, identification of L. monocytogenes and related organisms, and

for biosynthesis and biodegradation, especially biosynthesis of Vitamin

compounds that regulate gene expression and cell replication

and modulate L. monocytogenes—related diseases. In addition, the genome

compositions for the treatment or prevention of infections by L.

compocytogenes and related organisms.

compocytogenes and related organisms of the printed

specification, but was obtained in electronic format directly from WIPPO

at the mino in found in electronic format directly from WIPPO
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Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 16, 2003, 14:14:27 Job time : 35 secs
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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Gaps

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0; Indels

5; Conservative

512 YKWHG 516

3 YKWHG 7

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Listeria monocytogenes protein #1833

05-FEB-2002 (first entry)

ABB49129

BXBXBXB

ABB40129 standard; Protein; 552 AA

RESULT 15

ABB49129

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; Search time 12.3333 Seconds (without alignments) 30.875 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                          328717 segs, 42310858 residues
                                                                                                                   December 16, 2003, 14:11:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
                                                                                                                                                                                         US-09-870-089B-3
57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued
                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                 Scoring table:
                                                                             OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 2, Appli Sequence 31268, A Sequence 2, Appli Sequence 2, Appli Sequence 4341, Ap Sequence 11, Appl Sequence 11, Appl Sequence 5440, Ap Sequence 5470, Ap Sequence 25679, A Sequence 25679, A Sequence 2771, Ap Sequence 222, App Sequence 222, App Sequence 222, App Sequence 219, Appl 185, App 222, App 1219, App 182, App 89, Appl 90, Appl 91, Appl 92, Appl 90, Appl 91, Appl Sequence 13, Appl Sequence 330, App Description Sequence Sequence Sequence Sequence US-09-073-009-13 US-09-216-393B-330 US-08-84-153-2 US-09-252-991A-2820 US-09-282-203-2 US-09-282-203-2 US-09-282-125A-2 US-09-134-001C-4341 US-09-134-001C-4341 US-09-107-532A-6117 US-09-107-532A-6117 US-09-107-532A-6117 US-09-107-532A-6117 US-09-107-532A-6117 US-09-107-532A-6117 US-09-107-532A-6117 US-09-252-991A-2797 US-09-252-991A-2797 US-09-482-273-182 US-09-591-632-90 US-09-591-632-90 US-09-591-632-90 US-09-611-451-91 SUMMARIES DB Length Query Match Score Result No.

1 FLYKWHGF

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ce 92, Appl ce 183, App ce 120, App ce 119, App ce 5216, Ap ce 6294, Appli ce 4, Appli ce 4, Appli ce 4, Appli ce 4, Appli ce 4, Appli ce 2, Appli ce 30025, Appli ce 30025, Appli ce 435, Appli ce 435, Appli ce 435, Appli	TUBERCULOSIS	C; Gaps 0;
Sequence	э э э	Length 144; ; Indels
US-09-611-451-92 US-09-482-273-183 US-09-482-273-210 US-09-482-273-210 US-09-482-273-119 US-09-328-352-5216 US-09-328-352-5216 US-08-651-566A-4 US-08-661-566A-4 US-08-288-065A-4 US-08-288-065A-4 US-08-362-240A-4 US-08-362-240A-4 US-08-362-291A-31025 US-09-252-991A-31025 US-09-134-001C-4435 US-09-285-957-35	ALIGNMENTS 3009 inio s. AND DIAGNOSIS O r, 701 Fifth Ave. #1.0, Version #1 073,009 2 10121.441C1	tuberculosis Score 36; DB 4; Pred: No. 31; 1; Mismatches 2
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ALI  13-009-13  toe 13, Application US/09073009  18. No. 655563  19. LICANT: Alderson, Mark JUICANT: Skeiky, Yasir A.W. JUICANT: Compoures: 144  RESPONDENCE: 144  RESPONDENCE: 144  RESPONDENCE: Seed and BERRY  TYPE: Sattle  COMPUTE: Seattle  REDIUM TYPE: Floppy disk  COMPUTER: IBW PC Compatible  PERATUR SYSTEM: PC-DOS/MS-DOS  COMPUTER: IBW PC Compatible  PERATUR SYSTEM: PC-DOS/MS-DOS  COMPUTER: IBW PC-DOS/MS-DOS  COMPUTER: IBW PC-DOS/MS-DOS  COMPUTER: DatentIn Release #1.0  TLASSIFICATION DATE: US/09/073, 0  TLING DATE: 05-MAY-1998  COMPUTER: Maki, David J.  REJERRANT: David J.  REJERRANT: 206-622-4900  TRANDENDES: 206-622-4900  WATION FOR SEQ ID NO: 13: WATION FOR SEQ ID NO: 13: WATION COMPUTER: Single  TRANDEDNESS: single  PCOMPUTER: Deptide	cobacterium 63.2%; ity 62.5%; servative
6 6 6 8 8 8 9 9 9 8 9 9 9 9 9 9 9 9 9 9	SGULT 1  1-09-073-009-13  Sequence 13, Application US/Patent No. 6555653  GENERAL INFORMATION: APPLICANT: Alderson, MarAPLICANT: Alderson, MarAPLICANT: Seatky, Yasir APPLICANT: Seatky, Yasir APPLICANT: Seatky, Yasir APPLICANT: Seatle COWFUTEN: Seatle STREET: Sand COUNTRY: US  ZIP: 98104  COUNTRY: US  ZIP: 98104  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di COMPUTER: DE FORM: MEDIUM TYPE: PARTIN PROMATION APPLICATION NUMBER: US FILING DATE: 05-MAY-19 CLASSIFRCATION NUMBER: US FILING DATE: 05-MAY-19 CLASSIFRCATION NUMBER: US FILERAX: 206-682-490 TELEFAX: 206-682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 144 amino acid TYPE: amino acid TYPE: amino acid TYPE: Depotide TOPPOLOGY: linear	ORIGINAL SOUR ORGANISM: -073-009-13 ry Match t Local Simil
<u> </u>	RESULT SS - 09-T   SS - 09-T	j j US-09. Que: Besi Mate

AND M

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GENERAL INFORMATION:
APPLICANT: MARC J. RUDEnfield et al.
APPLICANT: MARC J. RUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31268
LENGTH: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28820, Application US/09252991A
Patent No. 6521795
REMERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABEUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28820
LENGTH: 463
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                                                                                       Score 36; DB 2; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 4; Length 463;
Pred. No. 1e+02;
2; Mismatches 2; Indels
                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                            Sequence 31268, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                    63.2%;
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55.6%;
                                                                                    Query Match 63.2
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 75.0
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Best Local Similarity 55.6
Matches 5; Conservative
                  ; MOLECULE TYPE: protein US-08-844-153-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 FRERWHGFL 314
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                       US-09-252-991A-31268
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                                                                                                  % Sequence 330, Application US/09216393B

% Sequence 330, Application US/09216393B

% Sequence 330, Application US/09216393B

% Datent No. 6514694

% GENERAL INFORMATION:
% APPLICATION
TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
% FILE REFERENCE: TX-1-C2
% CURRENT FILING DATE: 1998-12-18
% PRIOR APPLICATION NUMBER: 08/994,825
% CURRENT FILING DATE: 1997-12-19
% PRIOR PILING DATE: 1997-12-19
% NUMBER OF SEQ ID NOS: 366
% SOFTWARE: PatentIn version 3.1
% SEQ ID NO 330
% TENDOR 100 330
% TENDOR 100 330
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Pred. No. 43;
1; Mismatches 1; Indels
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SOPTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,153
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9607992.6
FILING DATE: 18-APR-1996
ATTORNEY, AGENY INPORMATION:
NAME: Gimmi, EGWARG R
REGISTRATION NUMBER: 38,891
REFERENTION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTRON: No. 5958734el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Baecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08844153
Patent No. 5958734
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19046
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Toxoplasma gondii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                134 FLCSWHGY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 LLRWHGF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
COUNTRY: USA
ZIE: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastesQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-273-142-2

Sequence 2, Application US/09273142

Patent No. 6300119

GENERAL INFORMATION:
APPLICANT: Jawlor, Elizabeth
APPLICANT: Wang, Min
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.2%; Score 36; DB 3; 362.5%; Pred. No. 1.1e+02; tive 1; Mismatches 2
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/962,203
FILING DATE: «Uhknown»
APPLICATION NUMBER: 9607992.6
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31459-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastsEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,142
                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,125A
FILING DATE: 07-Aug-2000
CLASSIFICATION: <UNKnown>
18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 480 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-1996
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 IYKWHDMV 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-282-125A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                      COMPUTER: PA

COMPUTER: PA

COMPUTER: 19406-0939

COMPUTER: Diskette

COMPUTER: Diskette

COMPUTER: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSED for Windows Version 2.0

SURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/962,203

FILING DATE: 31-0CT-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/844,153

FILING DATE: 18-APR-1997

APPLICATION NUMBER: 9607992.6

FILING DATE: 18-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Gimmi, SCHARATION:

NAME: COMMUNICATION NUMBER: 38,891

REFERENTION NUMBER: 38,891

REFERENTION NUMBER: 931459-1
                                              Sequence 2, Application US/08962203
; Patent No. 5976840
; CENERAL INFORMATION:
APPLICANT: Jaworski, Deborah
APPLICANT: Lawlor, Elizabeth
APPLICANT: Wang, Min
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jaworski, Deborah
Lawlor, Elizabeth
Wang, Min
TITLE OF INVENTION: NOVEL STREPTOCOCCAL ERS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09282125A Patent No. 6165760 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TONOLOGY: linear;
; MOLECULE TYPE: protein
US-08-962-203-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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159 IYKWHDMV 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-282-125A-2
                                    US-08-962-203-2
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECTUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                          Length 351;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                        61.4%; Score 35; DB 4; L
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 4; ]
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: (B) LÖCATION 1...472
; SEQUENCE DESCRIPTION: SEQ ID NO: 6117:
US-09-107-532A-6117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILING DATE: 30-JUL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6117, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: PC
OPERATING SYSTEM: <Unknown>
CURRENT FILING DATE: 2000-08-04
PRIOR APPLICATION UNDBER: 60/147,164
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 472 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 6117:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  TYPE: PRT
ORGANISM: Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.4%;
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      105 WHGFV 109
                                                                                                                                                                                                                                                                                                                             5 WHGFV 9
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Sequence 4341, Application US/09134001C

Sequence 4341, Application US/09134001C

Sequence 4341, Application US/09134001C

GENERAL INCORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1997-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
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Patent No. 6356845

GENERAL INCORMATION:
APPLICANT: Pharmacia & Upjohn

TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF

TITLE OF INVENTION: UDP-N-ACETYLENOLPYRUVYLGLUCOSAMINE REDUCTASE (S. aureus

TITLE OF INVENTION: MAID)

FILE REFERENCE: 268.6241 0101

CURRENT APPLICATION NUMBER: US/09/632,947B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 4; Pred. No. 1.1e+02; 1; Mismatches 2
                                                                                                                                                    P31459-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Staphylococcus epidermidis US-09-134-001C-4341
             FILING DATE:
APPLICATION NUMBER: 9607992.6
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,991
  APPLICATION NUMBER: 08/962,203
                                          9607992.6
                                                                                                                                           REFERENCE/DOCKET NUMBER: P3.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.2%;
                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 480 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                               610-270-5090
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 IYKWHDMV 166
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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GENERAL IN: 030230
GENERAL IN: 030230
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION TO ACID AND AMINOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5771
  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPREBACE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25679
LENGTH: 452
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 629
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Pred. No. 2.7e+02;
1; Mismatches 0; Indels
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Pred. No. 2.2e+02;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5771, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5771
                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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79 WHGFI 83
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US-09-252-991A-31575
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ORGANISM:
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                                                                                                                              RESULT 12
US-09-107-532A-5440
; Sequence 5440, Application US/09107532A
; Patent No. 6583276
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: BUTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: misc_feature
; CCATION: (B) LÖCATION 1...257
; SEQUENCE DESCRIPTION: SEQ ID NO: 5440:
US-09-107-532A-5440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25679, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                      STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (781)893-5007
TELEPK: (781)893-8277
INFORMATION FOR SEQ ID NO: 5440:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 257 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
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183 YLYRWH 188
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Best Local Similarity
Matches 4; Conserv
                                       1 FLYKWH 6
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11 YLFKWH 16
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Matches
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                                                   0; Gaps
Query Match 59.6%; Score 34; DB 4; Length 629; Best Local Similarity 80.0%; Pred. No. 3.1e+02; Matches 4; Conservative 1; Mismatches 0; Indels
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<sup>5</sup> WHGFV 9 ||||: 172 WHGFI 176

Search completed: December 16, 2003, 14:20:39 Job time : 13.3333 secs

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Sequence 5, Appli
Sequence 12, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 128, Ap
Sequence 123, App
Sequence 125, Ap
Sequence 126, Ap
Sequence 1475, Ap
Sequence 1475, Ap
Sequence 1475, Ap
Sequence 1476, Ap
Sequence 1706, Ap
Sequence 18, Appl
Sequence 11, Appl
Sequence 21, Appl
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09870089B
Publication No. US20030175252A1
GENERAL INFORMATION:
APPLICANT: Charles A. Nicolette
TITLE OF INVENTION: THERAPEUTC COMPOUNDS FOR OVARIAN CANCER
FILE REPRENDE: 68126881208700
CURRENT APPLICATION NUMBER: US/09/870,089B
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEO FOR Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09870089B
; Publication No. US20030175252A1
; GENERAL INFORMATION:
    APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
; FILE REFERENCE: 68126881209900
; CURRENT APPLICATION NUMBER: US/09/870,089B
105-09-443-704-12
105-09-443-704-12
4 US-10-068-1184-12
4 US-10-068-1184-12
5 US-10-156-761-8288
5 US-10-156-761-8288
6 US-09-991-211-11
5 US-10-156-761-10326
6 US-09-873-356-11
105-09-873-356-11
105-09-873-356-11
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105-09-138-686-3676
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105-09-705-365
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US-09-970-0898-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100
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US-09-870-089B-9
    Query Match
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Sequence 19, Appli
Sequence 19, Appli
Sequence 5220, Ap
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 130, App
Sequence 130, App
Sequence 1365, Ap
Sequence 1180, Ap
Sequence 1180, Ap
                                                                                                  2003, 14:18:11 ; Search time 22.1667 Seconds (without alignments) 75.512 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-09-870-089B-9
1 US-09-791-279-198
US-09-870-089B-7
5 US-10-106-698-5220
US-09-073-009-13
US-09-073-006-13
US-09-793-306-13
US-09-793-306-13
US-09-16-245-330
US-09-185-242-13455
US-09-925-299-1180
US-09-815-248-12
US-09-815-248-12
US-09-815-248-12
US-09-815-248-12
US-09-815-248-12
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                                                                                                                                                                                                                                                                       684280 seqs, 185983659 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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57
1 FLYKWHGFV 9
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1194
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Match Length
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Gaps

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US-09-870-089B-7
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                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 12; Length 9;
Pred. No. 6.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NO. US20030050456A1E1 COURENT APPLICATION WINDER: US/09/791,279 CURRENT APPLICATION WUNDER: US/09/791,279 CURRENT FILING DATE: 2000-02-24 PRIOR FILING DATE: 2000-02-24 PRIOR FILING DATE: 2000-02-24 PRIOR PELLING DATE: 2000-02-24 PRIOR PELLING DATE: 2000-02-24 PRIOR FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: 60/184,716 PRIOR APPLICATION NUMBER: 60/184,716 PRIOR FILING DATE: 2000-02-24 PRIOR FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: 60/184,716 PRIOR FILING DATE: 2000-02-24 PRIOR
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 198, Application US/09791279
Publication No. US20030050456Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                    FEATURE:
CTHER INFORMATION: ATF4/CREB-2
US-09-870-089B-9
                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                               71.9%;
66.7%;
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APPLICANT: Wood, Linda S.
APPLICANT: Parodi, Luis
APPLICANT: Lind, Peter
                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.9
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
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1 FLHKWHWYV 9
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84 FLNLWHGFL 92
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LENGTH: 220
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RESULT 4

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US-10-10-508-5220

Sequence 5220, Application US/10106698

Sequence 5220, Application US/10106698

Publication No. US2030109690A1

GENERAL INFORMATION:

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

FILE REFERENCE: PA005P1

FILE REFERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: P6/150/137

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR PILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SEQ ID NO 5220

LENGTH: 22
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Sequence 7, Application US/09870089B; Publication No. US20030175252A1; GENERAL INFORMATION:
APPLICANT Charles A. Nicolette; TILLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER; TILLE REFERENCE: 68126881209900; CURRENT APPLICATION NUMBER: US/09/870,089B; CURRENT FILING DATE: 2001-05-30; NUMBER OF SEQ ID NOS: 14; SOUTHARE FastSEQ for Windows Version 3.0; SEQ ID NO 7; SEQ ID NO 7; LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
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Pred. No. 6.1e+05;
1; Mismatches 2; Indels
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Patent No. US20010012888A1
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: ATF4/CREB-2
US-09-870-089B-7
                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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US-10-106-698-5220
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LFKWHNF 12
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APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Ovendale, Pamela
APPLICANT: Ovendale, Pamela
APPLICANT: Ovendale, Pamela
APPLICANT: Gorixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: Of Tuberculosis
FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR PILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR PILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGHIH: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 330, Application US/09216393
Patent No. US2001001447A1
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
                                                                                                                                                                                                                                                       63.2%; Score 36; DB 9; Length 144; 62.5%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.2%; Score 36; DB 9; Length 144; 62.5%; Pred. No. 1.5e+02; 1ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                    TOPOLOGY: linear MolECULE TYPE: peptide
CORGINAL SOURCE:
CREANISM: Mycobacterium tuberculosis
US-09-023-588-13
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LOCATION: (1)...(144)

OTHER INFORMATION: Xaa = any amino acid
US-09-793-906-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09793306
Patent No. US200200098200A1
GENERAL INFORMATION:
APPLICANT: Campos-Neto, Antonio
      (206) 622-4900
                                                                            LENGTH: 144 amino acids
TYPE: amino acid
STRANDEDNESS: Bingle
TOPOLOGY: linear
                    TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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OTHER INFORMATION: Tb224
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US-09-216-393-330
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US-09-793-306-13
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Patent No. US2002001579A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark R.
TILLE OF INVENTION: METHOD FOR THE ISOLATION OF NOVEL ANTIGENS NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.2%; Score 36; DB 9; Length 144; 62.5%; Pred. No. 1.5e+02; tive 1; Mismatches 2; Indels
                                                                              ZIP: 98104
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,588
FILING DATE: 14-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ADDRESSEE: SEED and μμκι.
STREET: 6300 Coumbia Center, 701 Fifth Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.445
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || |||:
|34 FLCSWHGY 141
                                                            Washington
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Best Local Similarity
Matches 5; Conserv
                STREET: boc.
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US-09-023-588-13
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LOCATION: (42)
OCHBR INPORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (75)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (81)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Fatent No. US20020055627A1;
GENERAL INFORMATION:
TITLE OF INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299;
CURRENT FILING DATE: 2001-08-10;
FRIOR PAPLICATION NUMBER: PCT/US00/05883;
FRIOR APPLICATION NUMBER: PCT/US00/05883;
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR PILING DATE: 1999-03-12;
NUMBER OF SEQ ID NOS: 1556;
SOFTWARE: PatentIn Ver. 2.0;
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 9; Length 486; Pred. No. 4.5e+02; 1; Mismatches 2; Indels
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                     PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PRILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTWARE: FastSEQ for Windows Version 4.0
SEROIT 486
                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pneumoniae US-09-815-242-13455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
       FILING DATE: 2000-05-23
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165 IYKWHDMV 172
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ORGANISM: Homo sapiens
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LOCATION: (95)
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TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
FILE REPERENCE: TX:1-C2-1
CURRENT APPLICATION NUMBER: US/10/321,856
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR APPLICATION NUMBER: 09/94,825
PRIOR APPLICATION NUMBER: 09/94,825
PRIOR RILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
SEQ ID NO 330
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Pred. No. 2e+02;
1; Mismatches 1; Indels
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: 1201-03-21
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                        Score 36; DB 9; Length 197;
Pred. No. 2e+02;
1; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/994,825
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 330, Application US/10321856 Publication No. US20030194393A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative 1
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Best Local Similarity 71.4%;
Matches 5; Conservative
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; ORGANISM: Toxoplasma gondii
US-10-321-856-330
                                                                                                                                                                                                                                    ORGANISM: Toxoplasma gondii
US-09-216-393-330
                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 LLRWHGF 179
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us-09-870-089b-3.rapb

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Gaps

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Query Match 61.4%; Score 35; DB 9; Length 99; Best Local Similarity 75.0%; Pred. No. 1.6e+02; Matches 6; Conservative 0; Mismatches 2; Indels
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ORGANISM: Artificial Sequence
FEATURE:
  ; ORGANISM: Drosophila sp. US-09-815-248-12
                                                                                                                                                                                       13 LYIWHKFV 20
                                                                                                                                               2 LYKWHGFV 9
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140 MYQWHG 145
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Patent No. US20020098540a1

GENERAL INFORMATION:
APPLICANT: RASTELL, LUCA
APPLICANT: PENNICA, DIANE
TITLE OF INVENTION: NOVEL POLYPEPTIDES, AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: 10716.36
CURRENT FILING DATE: 2001-08-20
PRIOR PILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEATURE:
NAME/KEY: SITE
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (50)
LOCATION: (50)
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OFFER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OFFER INFORMATION: (75)
OFFER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (81)
LOCATION: (81)
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APPLICANT: ROBERTON:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299; CURRENT FILING DATE: 2001-08-10; PRIOR APPLICATION NUMBER: PCT/US00/05883; PRIOR PILING DATE: 2000-03-08; PRIOR PILING DATE: 1999-03-12; NUMBER OF SEQ ID NOS: 1556; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.4%; Score 35; DB 11; Length 96; 83.3%; Pred. No. 1.5e+02;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 5; Conser
                                     69 YKWQGF 74
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3 YKWHGF 8
                                                                                                      RESULT 13
US-09-925-299-1180
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US-09-815-248-12
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APPLICANT: Glucksmann, Maria A. APPLICANT: Galvin, Katherine M. APPLICANT: Galvin, Katherine M. TITLE OF INVENTION: 41449, 50289, 528172 AND 265908 MOLECULES AND USES THEREFOR FILE OF INVENTION: 41449, 50289, 528172 AND 265908 MOLECULES AND USES THEREFOR GURERNT APPLICANTON NUMBER: US 10/226,102 PRIOR APPLICANTON NUMBER: US 10/226,102 PRIOR APPLICANTON NUMBER: US 60/314,041 PRIOR APPLICANTON NUMBER: US 60/314,041 PRIOR APPLICANTON NUMBER: US 60/314,185 PRIOR FILING DATE: 2002-08-22 PRIOR FILING DATE: 2001-08-22 PRIOR FILING DATE: 2001-08-22 PRIOR FILING DATE: 2002-09-16 PRIOR FILING DATE: 2002-09-17 PRIOR APPLICANTON NUMBER: US 60/314,185 PRIOR FILING DATE: 2002-10-15 PRIOR APPLICANTON NUMBER: US 60/314,185 PRIOR FILING DATE: 2002-11-17 PRIOR APPLICANTON NUMBER: US 60/314,185 PRIOR APPLICANTON NUMBER: US 60/314,185 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICANTON NUMBER: US 60/314,185 PRIOR FILING DATE: 2000-10-24 PRIOR FILING DATE: 2000-02-24 PRIOR FILING DATE: 2000-02-29 PRIOR APPLICANTON NUMBER: US 60/186,059 PRIOR FILING DATE: 2000-02-29 PRIOR FILING DATE: 2000-02-29 PRIOR FILING DATE: 2000-02-29 PRIOR PRIOR APPLICANTON NUMBER: US 60/186,059 PRIOR FILING DATE: 2000-02-29 PRIOR PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Amino acid consensus sequence
                                                                                                                                                              APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: December 16, 2003, 14:41:05 Job time: 22.1667 secs
Sequence 109, Application US/10407079
Publication No. US20030215860A1
GENERAL INFORMATION:
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Title:

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                                                                           bacillus su
spinacia ol
dictyosteli
           kluyveromyc
escherichia
                             homo sapien
                                        mus musculu
                                                                                                         epstein-bar
                                                         pseudomonas
                                                 rattus norv
                                                                   arbacia lix
                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 24:4420-4449(1996).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                  "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MG015 homolog
                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
NCBL_TaxID=2104;
                           075712
P2831
P25305
Q51548
P34941
006005
Q9sek3
P36418
P03227
          O60014
P76363
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; FubMed=6948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FP (POTENTIAL).
E10CE07E0EBBD406 CRC64;
                                                                                                                                     ALIGNMENTS
 HCYC EURCA
UBRI KLUIA
YEET ECCLI
CXB3 HDWAN
CXB3 MOUSE
CXB3 RAT
PUDA ARBLI
NU4M ARBLI
AARA BACSU
AARA BACSU
VILLI SPIOL
VILLI SPIOL
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  (D12 orf634).
MPN019 OR MP135.
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ID Y015 MYCPN
AC P75094;
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                                                              December 16, 2003, 14:06:35; Search time 5.6667 Seconds (without alignments) 74.689 Million cell updates/sec
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P55653
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Q97ng1
Q86vx9
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Copyright (c) 1993 - 2003 Compugen Ltd.
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HCYG ENCA

DCOR ECOLI

YJ9G YEAST

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LSPA ECOST
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Maximum Match 100%
Listing first 45 summaries
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ADVL MOUSE
SYQ BUCAI
YO15 MYCGE
SYW FYRAE
GABD RHISN
CCS CITSI
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- TISSUE SPECIFICITY: MOST HIGHLY EXPRESSED IN THE ENDOMETRIUM OF THE UTERUS, THE INTESTINAL VILLI AND THE TEGTES. WEAKER EXPRESSION ALSO DETECTED IN THE BRAIN AND ON THE SURFACE OF THE TONGUE.

-i- DEVELOPMENTAL STAGE: HIGHEST EXPRESSION WAS DETECTED IN DORSAL ROOT AND TRIGEMINAL GANGLIA BY EMBRYONIC DAY 14.5 AND CONTINUED THROUGH AT LEAST DAY 16.5.

-i- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NIH Swiss;
MEDLINE=98315054; PubMed=9649432;
MEDLINE=98315054; PubMed=9649432;
MEDLINE=98315054; PubMed=9649432;
MIDLINE=98315054; PubMed=9649432;
Sinszner H., Ron D.;
"Identification of novel stress-induced genes downstream of chop.";
EMBO J. 17:5619-3630 (1998).
-!- FUNCTION: CA.(2+) - REGULATED ACTIN-BINDING PROTEIN. MAY HAVE A
-!- UNIQUE PUNCTION IN THE MORPHOGENESIS OF NEURONAL CELLS WHICH FORM
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=89330437; PubMed=5664034;
Marks P.W., Arai M., Bandura J.L., Kwiatkowski D.J.;
Advillin (p92): a new member of the gelsolin/villin family of actin regulatory proteins.";
                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; revology VHP; 1.
Pfam; PF02209; VHP; 1.
PRINTS; PR00597; GEL50LIN.
SMART; SM00152; GEL; 6.
SMART; SM00153; VHP; 1.
Cytoskeleton; Calcium; Actin-binding; Capping protein; Repeat.
                                   ·;
70.2%; Score 40; DB 1; Length 634; 55.6%; Pred. No. 13; ive 2; Mismatches 2; Indels
                                                                                                                                                                                   ADVL_MOUSE STANDARD; PRT; 819 AA. 088398; O70466; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 18-ERE-2003 (Rel. 41, Last annotation update) Advillin (p92) (Actin-binding protein DOC6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P02640; ZVIL.
MGD; MG1:1333798; Avil.
MGC; MG:0006950; P:response to stress; IDA.
InterPro; IPR001974; Gelsolin.
InterPro; IPR003128; VHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulatory proteins.";
J. Cell Sci. 111:2129-2136(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF041448; AAC25050.1; -. EMBL; AF059486; AAC31808.1; -.
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Pfam; PF02209; VHP; 1.
                                   5; Conservative
                                                                                        297 FIXSWEGFI 305
                                                                     1 FLYKWHGFV 9
               Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLNS OR BU415.
Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mature 407:81-86(2000).
Nature 407:81-86(2000).
-!- CATALYTIC ACTIVITY: ATP + L-glutamine + tRNA(Gln) = AMP +
dlphosphate + L-glutaminyl-tRNA(Gln).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELULIAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20445173; PubMed=10993077; Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.; "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
Glutaminyl-tRNA synthetase (EC 6.1.1.18) (Glutamine--tRNA ligase)
(GlnRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Buchnera.
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                                                                                                                           POLYPHOSPHOINOSITIDE BINDING (BY SIMILARITY).
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R - 5 (IN REF. 2).
I - N (IN REF. 2).
R - 5 (IN REF. 2).
W; 88CD9DBDEDF1F77D CRC64;
             GELSOLIN-LIKE 2
GELSOLIN-LIKE 3
GELSOLIN-LIKE 4
GELSOLIN-LIKE 5
GELSOLIN-LIKE 5
VHP.
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InterPro; IPR004514; dlnS.
InterPro; IPR004514; dlu ENNA-synt_1c.
InterPro; IPR001412; tRNĀ-synt_1.
Pfam; PF00749; tRNA-synt_1.
Pfam; PF003950; tRNA-synt_1c. C; 1.
PRINTS; PR00987; TRNA-SYNTHGIU.
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                                                                                                                                                                                                                                                               92186 MW;
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Matches 5; Conservative
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819 AA;
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Miller J.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Frieschman D.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Wiguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M. Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
TIGRFAMS; TIGR00440; glnS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                       Gaps
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0
                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probom, PD000006; ABC transporter; 1.
SWART; SW0382; AAA; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
Hypothetical protein; ATP-binding; Transport; Transmembrane;
                                                                                                          Score 38; DB 1; Length 571;
Pred. No. 26;
                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
Hypothetical ABC transporter ATP-binding protein MG015.
                                                           "KMSKS" REGION.
ATP (BY SIMILARITY).
1FCE69932D563D52 CRC64;
                                                                                                                                    0; Mismatches
                                                  "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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Interpro; IPR001393; AAA ATPase.
Interpro; IPR001140; ABC_TM_transpt.
Interpro; IPR003439; ABC_transporter.
Pfam; PP00064; ABC_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; Pubmed=7569993;
                                                                                    571 AA; 67835 MW;
                                                                                                            66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U39680; AAC71231.1; -. PIR; F64201; F64201.
                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                               STANDARD;
                                                  45
273
272
                                                                                                                                                                                                                                                                                                                                  Mycoplasma genitalium.
                                                                                                                                                                                  92 YKWHGNV 98
                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                            3 YKWHGFV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P13569; INBD.
                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
                                                  35
269
272
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                      01-FEB-1996 (
01-FEB-1996 (
16-OCT-2001 (
                                                                                                                                                                                                                                               YO15 MYCGE
                                                                                    SEQUENCE
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TRANSMEM
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                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
-!- CATALYTIC ACTYUTY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
-!- SUBCELLUTAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Typtophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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                                                                                                     Score 38; DB 1; Length 589;
Pred. No. 27;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37, DB 1, Length 375, Pred. No. 27, 1; Mismatches 1; Indels
  POTENTIAL.
ATP (POTENTIAL).
0EA6A816DD3A3CC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBL_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "KMSKS" REGION.
3DDBF85DA680F116 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF_00140; -; 1.
InterPro; IPR001305; tRNA-synt_lb.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR002306; Trp_tRNA-synt_lb.
Pfam; PF00579; tRNA-synt_lb; 1.
PRINTS; PR01039; TRNASYNTHTRP.
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PROSITE; PS00178; AA TRNA LIGASE I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523,
MEDLINE=21664397; PubMed=11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE009911; AAL64664.1; -.
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                                                     66126 MW;
                                                                                                        66.7%;
55.6%;
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                                                                                                     Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
  323
392
                                                                                                                                                                                                                                                        252 FLFSWFGFI 260
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                                                                                                                                                                                                           1 FLYKWHGFV 9
303
385
589 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRPS OR PAE3091
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Xu C.J., Chen D.M., Zhang S.L.;
"Molecular cloning of capsanthin/capsorubin synthase gene from orange (Cittus sinensis).";
submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE CONVERSION OF THE UBIQUITOUS 5,6-
BPOXYCAROTENOIDS, ANTHERAXANTHIN AND VIOLAXANTHIN, INTO CAPSANTHIN
AND CAPSORUBIN, RESPECTIVELY.
                                                                                                                                                                                                                                                              Transit peptide
                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGPD DROYA
                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                 NP BIND
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G6PD DROYA
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Sapindales, Rutaceae, Citrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)
                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
                                                                                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: Succinate semialdehyde + NAD(P)(+) + H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                               "Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
                                                                                                                                    Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.9%; Score 37; DB 1; Length 491; 62.5%; Pred. No. 34; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FC54C5DF7B4D1B14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CGS-cgpsanthin/capsorubin synthase, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P05091, 1CM3.
InterPro; IPR02086; Aldehyde_dehydr.
Pfam; PF00171; aldedh; AlbehyDe_DEHYDR_CYS; FALSE_NEG.
PROSITE; PS000070; ALDEHYDE_DEHYDR_CYS; FALSE_NEG.
Oxidoreductase; NADP; Plasmid.
                                                                                                                                                                                                                                                                                              -!- PATHWAY: 4-aminobutyrate (GABA) degradation.
                          491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
BY SIMILARITY
                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Citrus sinensis (Sweet orange).
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000096; AAB91849.1; -. PIR; S43963; S43963.
                                                                                                                         (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53253 MW;
                                                                                                                                                                                                                                                                                  succinate + NAD(P)H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 LWKWHRFI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LYKWHGFV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     491 AA;
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NCBL TaxID=2711;
                                                                                                                                                                         NCBI_TaxID=394;
                                                                                                           GABD OR Y4SJ.
                                                                                                                        Rhizobium sp.
                        GABD RHISN
P55653;
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ACT_SITE
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Q9SEA0;
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                                                                                                                                                                                                                                                           Nature
                GABD_RHISN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BG1016;
Eanes W.F., Kirchner M., Yoon J., Biermann C., Wang I., McCartney M., Verrelli B.C.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FKB-2003 (Rel. 41, Last annotation update)
Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD) (Fragment)
-!- PATHWAY: Carotenoid biosynthesis.
-!- SUBCELLULAR LOCATION: Chloroplast; chromoplast (By similarity).
-!- SIMILARITY: BELONGS TO THE LYCOPENE CYCLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucc
1,5-lactone 6-phosphate + NADPH.
-!- PATHWAY: Pentose phosphate pathway; first step.
-!- SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
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O
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAPSANTHIN/CAPSORUBIN SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF169241; AAF18389.1; -.
Oxidoreductase; NAD; Carotenoid biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2C957F0AA91075E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHLOROPLAST (POTENTIAL)
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Pred. No. 35;
1; Mismatches
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Drosophila yakuba (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U42750; AAB02813.1; -.
HSSP; P11411; 1DPG.
FlyBase; FBgn0015691; Dyak\Zw.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 64.9%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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503
117
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AE003512; AAF48999.1;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20196066; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamsides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amaratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
N. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen Lix,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Anni J.F., Aspayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,
Borkova D., Botchan M.R., Bourd J., Brocketein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=F23.3, F24.1, MT41, MT68, Z3, Z5, Z11, Z16, Z21, Z27, Z41, Z42, Z55, Z62, Z64, and Z74;
MEDLINE=97070821; PubMed=8913747;
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eanes W.F., Kirchner M., Yoon J., Biermann C.H., Wang I.N., McCartney M.A., Verrelli B.C.; "Historical selection, amino acid polymorphism and lineage-specific divergence at the Gépd locus in Drosophila melanogaster and D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88255872; PubMed=2838391;
Fouts D., Ganguly R., Gutierrez A.G., Lucchesi J.C., Manning J.E.;
"Nuclectide sequence of the Drosophila glucose-6-phosphate
dehydrogenase gene and comparison with the homologous human gene.";
Gene 63:261-275(1988).
                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha; Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                    64.9%; Score 37; DB 1; Length 518; 100.0%; Pred. No. 36; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                              GGPD_DROME STANDARD, PRT, 524 AA.
P12646; Q27574; Q27872; Q27879; Q27881; Q9VWE3; Q9VWE3; O1-0CT-1989 (Rel. 12, Created)
15-UUL-1998 (Rel. 21 Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glucose-6-phosphate 1-dehydrogenase (BC 1.1.1.49) (G6PD)
                                                                                                               203 203 BY SIMILARITY.
518 AA; 59938 MW; 6AFA194E1D3A3E8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
            Pfam; PF04479; G6PD; 1.
PRIAM; PF02781; G6PD_C; 1.
PRINTS; PR00079; G6PDHDRGNASE.
ProDom; PD001129; G6PD; 1.
TIGREAMS; TIGROOGT1; 24F; 1.
PR051TF; PS00069; G6P DEHYDROGENASE; 1.
Oxidoreductase; NADP; Glucose metabolism.
                                                                                                                                                                                                                                                                                                                                                                                        ZW OR GGPD OR CGi2529. 
 Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics 144:1027-1041(1996).
InterPro; IPR001282; G6PD.
                                                                                                                                                                 Local Similarity 100.
es 5; Conservative
                                                                                                                                                                                                                                  506 YKWHG 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                         3 YKWHG 7
                                                                                                                                                                                                                                                                                                                                                                             (Zwischenferment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Berkeley;
                                                                                                                 ACT_SITE
SEQUENCE
                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              simulans.
                                                                                                      NON TER
                                                                                                                                                                                                                                                                                   G6PD_DROME
                                                                                                                                                                               Matches
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Gordek A., Gorrell J.H., Gu Z., Gana P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wei M.-H., Hoeyam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., Mosherson D., Markulov G., Milshian N.V., Mobarry C., Morris J., Mosherefi A., Melson D.R., Moy M., Murphy B., Murphy D., Murry D.M., Nelson D.L., Ra Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Sauder K., Sauder K., Scheler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shiese B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Ang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Nan G., Zhan M., Zhang G., Zhao Q., Zhao G., Zheng I., Zhong X., Myer B.W., Myere E.W., Wang S., Yao Q.A., Zheng X., Myere S.W., Woodege T., Worley K.C., Wu D., Yang S., Yao Q., Zheng I., Zhong X., Myere S.W., Woodes E.W., Wootes E.W., Kubin G.M., Venter J.C.; The Gonome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22426066; PubMed=12537569; Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., Garlson J.W., Brokstein P., Yu C., Champe M., Garlson J.W., Brokstein P., Yu C., Champe M., Garin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H., Rubin G.W., Celniker S.E.; Desource."; A Drosophila full-length cDNA resource."; Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
-!- CATALTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isoid=Pl2646-2; Sequence=VSP 001593;
Note=No experimental confirmation available;
SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1,5-lactone 6-phosphate + NADPH.
-!- PATHWAY: Pentose phosphate pathway; first step.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Long;
Isold=P12646-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM LONG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M26674; AAA51463.1; -.
EMBL; M26673; AAA51463.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB02805.1;
AAB02806.1;
AAB02807.1;
AAB02808.1;
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AAB02804.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U42739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U42740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U42741;
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EMBL;
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modified and this statement is not removed.
                                                                                                                                                                                                                                 162 YKWHG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=36870;
                                                                                                                                                                                                            3 YKWHG 7
                                                                                                                                                                                                                                                                                        LSPA WIGBR
QBD2R1;
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                   RESULT 11
LSPA WIGBR
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Matches
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                                                                                                                                                                     BY SIMILARITY.

Missing (in isoform Short).

/FIId=VSP 001593.

G -> C (IN STRAINS F24.1, MT32 AND MT68).

T -> N (IN STRAINS F23.3, MT41, Z3, Z5, Z11, Z16, Z21, Z27, Z42, Z55, Z64, Z74, AND BERKELEY).

QA -> AG (IN REF. 1).

N -> K (IN REF. 1).

LGV -> AAAQ (IN REF. 1).

DELRE -> AAAQ (IN REF. 1).

MW; ABF81LB763A82FIFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
-!- FUNCTION: Relaxes both positive and negative superturns and exhibits a strong decatenase activity. The B subunit binds ATP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATAINTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
TYPE II DNA topoisomerase VI subunit B (EC 5.99.1.3) (TopoVI-B).
                                                                                                                                                                                                                                                                                                                                                         ..
64.9%; Score 37; DB 1; Length 524; 100.0%; Pred. No. 36; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \label{eq:similarity} \mbox{$\text{-i-similarity}$.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                         527 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                          524 AA; 60431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoproteaceae; Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  512 YKWHG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                             3 YKWHG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPGB PYRAE
Q8ZVMO;
                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                    VARIANT
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loved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                HAMAP, MF 00322, -; 1.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IRR005794; DNA topEB.
Pfam; PF02518; HATPase c; 1.
SMART; SM00387; HATPase c; 1.
TIGRFAMs; TIGR01052; topEb; 1.
ISOMERAS; Topoisomerase; DNA-binding; ATP-binding; Complete proteome.
SEQUENCE 527 AA; 59870 MW; 7BAADB81F8FC9D97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Files, Wigglesworthia glossinidia.";

Nat. Genet. 32:402-407(2002).

-- FUNCTION: This protein specifically catalyzes the removal of signal peptides from prolipoproteins (By similarity).

-- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from membrane prolipoproteins. Hydrolyses Xaa. Xbb. Xcc. | -Cys, in which Xaa is hydrophobic (preferably Leu), Xbb is often Ser or Ala, Xcc is often Gly or Ala, and the Cys is alkylated on sulfur with a diacylglyceryl group.

-- SUBCELLUIAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22297718; PubMed=12219091;
Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-5E2-2003 (Rel. 42, Created)
15-5EP-2003 (Rel. 42, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal peptidase) (Signal peptidase II) (Spase II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wigglesworthia glossinidia brevipalpis.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of the endocellular obligate symbiont of tsetse
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Aspartyl protease; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                       64.9%; Score 37; DB 1; Length 527, 100.0%; Pred. No. 36; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Probable).
SIMILARITY: Belongs to peptidase family A8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 AA
                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAR; MF 00161; -; 1.
InterPro; IPR001872; SigPTase A8.
Pfam; PF01222; Peptidase A8; 1.
PRINTS: PR00781; LIPOSIGFTASE.
ProDom; PD004304; SigPTase A8; 1.
TIGRRAMS; TIGR00077; 18pA; 1.
PROSITE; PS00855; SPASE II; FALSE NEG.
                                                                                    EMBL; AE009863; AAL64036.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB063521; BAC24439.1; -.
                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
1es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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us-09-870-089b-3.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-ATCC 15692 / PAO1;
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody E.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
MEDLINE-ATCC 15692 / PAO1;
MEDLINE-ATCC 15692 / PAO1;
MEDLINE-ATCC 15692 / PAO1;
MEDLINE-ATCC 15692 / PAO1;
M. Filloux A., Akrim M., Ball G., Lazdunski A., Tommassen J.;
Mencin secretion in Pseudomonas acruginosa: characterization of
seven xcp genes and processing of secretory apparatus components by
prepilin peptidase.";
Mol. Microbiol. 6:1121-1131(1992).
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTYEINS, REQUIRED FOR THE TRANSLOCATION OF A VARIETY OF ENZYMES ACROSS THE OUTER MEMBRANE.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
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                                                                                                                                                                                                                                                                               63.2%; Score 36; DB 1; Length 153; 66.7%; Pred. No. 17; 1.1ve 2; Mismatches 0; Indels
                                                                                                                  Potential.
BY SIMILARITY.
BY SIMILARITY.
1 1AEB3B201B935B58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DBC-1992 (Rel. 24, Created)
01-DBC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405 AA.
                       Potential.
Potential.
Potential.
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Interpro; IPR001992; Bact_secr_systII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         General secretion pathway protein F. XCPS OR PA3102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                       7 24 POI
60 79 POI
86 108 POI
123 145 POI
135 105 BY
135 AA; 18085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE004734; AAG06490.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X62666; CAA44534.1; -.
                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406:959-964 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S25385; SKPSXS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 YIYKWH 124
                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               1 FLYKWH 6
Complete proteome
TRANSMEM 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPF_PSEAE

AC G00517

DT G005717

DT 01-DEC-1992

DT 01-DEC-1992

DT 01-DEC-1992

DT 01-DEC-1992

DT 01-DEC-1992

DT 01-DEC-1992

DT General secre

GN CCPS OR PA310

SECONDORE FROM

RP SECONDORE FROM

RP SECONDORE FROM

RR SECONDORE FROM

RR BAILY M., File

RA BAILY M., File

RA BAILY M., File

RA BAILY M., File

RA Garber R.L.,

CC Mandle Google

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ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi S.H., Leach J.E.; "Identification of the XorII methyltransferase gene and a ver homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from Xanthomonas oryzae pv. oryzae.";
Mol. Gen. Genet. 244:383-390(1994).
-!- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG, CAUSES SPECIFIC METHYLATION ON C-? ON BOTH STRANDS AND PROTECTS THE DNA FROM CLEAPAGE BY THE XORII ENDONUCLEASE.
-!- CATALYTIC ACTIVITY: 9-adenosyl-L-methionine + DNA cytosine = S-adenosyl-L-homocysteine + DNA 5-methylcytosine.
-!- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonas oryzae (pv. oryzae).
Bacteria; Froteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Modification methylase XorII (EC 2.1.1.73) (Cytosine-specific methyltransferase XorII)
Pfam; PP00482; GSPII_F; 1.
PRINTS; PR00812; BCTERLALGSPF.
PROSTTE; PS00874; T2SP_F; 1.
Transport; Transmembrame; Inner membrane; Complete proteome.
                                                                                                                                                                                                                                                                               63.2%; Score 36; DB 1; Length 405; 55.6%; Pred. No. 42;
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                                                                                                                                                                                                                                                                                                                                             2; Indels
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HSSP; P20569; IDCT.
REBASE; 3534; M.XorII.
REPASE; 1534; M.XorII.
REPASE; PR00145; DNA_meth, PEAM; PF00145; DNA_meth, PR00145; DNA_meth, PR00145; DNA_meth, PR00178; PR00105; CSMETRREASE.
TIGRRAMS; TIGRROGOS; CS_MTASE 1; 1.
PROSITE; P800094; CS_MTASE 1; 1.
PROSITE; P800095; CS_MTASE 2; 1.
Transferase; Methyltransferase; Restriction system.
ACT_SITE
83 BY SIMILARITY.
SEQÜENCE 424 AA, 46971 MW; F2EEB12F09918781 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F2EEB12F09918781 CRC64;
                                                                                                                                                                                                                     405 AA; 44061 MW; BEE59B58724C167E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 AA.
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                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                              POTENTIAL.
                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=JW89011;
MEDLINE=94359461; PubMed=8078464;
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                              189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 FRERWHGFL 256
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wes 5; Conserve
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219
377
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       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBLEM PRO0749; TRNA-Synt. 1C; 1.
PRINTS; PRO0987; TRNASYWTHGLU.
TIGRFAMS; TIGRO0464; gltx. Bact; 1.
PROSTIE; PS00178; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).

-!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP + diphosphate + L-glutamy!-tRNA(Glu).

-!- SUBJUNIT: Monomer (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to class-I aminoacy!-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                          15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sentencion update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
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                                                                                                                                                                                                                                                                                                                                                   Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       485 AA; 55720 MW; DFA1E99D0CD1363F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "KMSKS" REGION.
ATP (BY SIMILARITY).
                                                                                                                                                                 485 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=UAIS9 / ATCC 700610 / Serotype C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAWAR; MF 00022; -; 1.
InterPro; IPR004527; GltX bact.
InterPro; IPR00924; Glu tRNA-synt_IC.
InterPro; IPR01412; FNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22295063; PubMed=12397186
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ID SYE STRPN STANDARD; F

AC 097NG1;

DT 15-SEP-2003 (Rel. 42, Created)
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                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 IYKWHDMV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LYKWHGFV 9
                                              337 KWHGF 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 5; Conserv
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KWHGF 8
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                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC BAA-334 / TIGR4;

MEDLINE=2135-209; PubMed=11463916;

Tettelin H., Nelson R.E., Paulsen I.T., Eisen J.A., Read T.D.,

Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,

Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,

Holtzapple B., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

McDonald L.A., Peldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,

Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam: PF00749; tRNA-synt 1c; 1.
PRINTS; PR00897; TRNASYNTHGIU.
TIGRFAMs; TIGR00464; gltx_bact; 1.
PROSITE; PS00178; AA TRNA_LIGASE 1; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i - CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP + diphosphate + L-glutamyl-tRNA(Glu).
-i - SUBUNIT: Monomer (By similarity).
-i - SUBCELLUTAR LOCATION: Cytoplasmic.
-i - SUBCELLUTAR LOCATION: Cytoplasmic.
-i - SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                         Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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ATP (BY SIMILARITY)
72EF5FDF704B3011 CRC64;
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Job time : 6.66667 secs
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InterPro; IPR004527; Gltx_bact.
InterPro; IPR004527; Glu ERNA-synt_Ic.
InterPro; IPR00412; tRNĀ-synt_I.
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Science 293:498-506(2001)
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259
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Best Local Similarity
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                                                                                                                                                                                                                                             Streptococcus.
NCBI_TaxID=1313;
                                                                                                                                        GLTX OR SP2069.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 16, 2003, 14:09:45 ; Search time 25 Seconds (without alignments) 92.899 Million cell updates/sec Run on:

US-09-870-089B-3 Perfect score: Title:

1 FLYKWHGFV 9 **BLOSUM62** Scoring table: Seguence:

830525 seqs, 258052604 residues

Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

830525

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 23:\* Database :

sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\* sp\_rvirus:\*
sp\_bacteriap:\* sp\_organelle:\* sp\_archea:\* sp\_bacteria:\* sp plant:\* fungi:\* sp\_fungi:\* 11; 12; 13; 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

STIMMARIES

	Description	Q27598 drosophila	Q9v896 drosophila	Q9y0b3 sarcophaga	044249 manduca sex	Q9aw53 guillardia	Q8xil5 clostridium	Q8ilp5 plasmodium	Q95r43 drosophila	Q9w1v6 drosophila	Q8i1f6 drosophila	Q9blg6 bombyx mori	Q9gu90 bombyx mori	Q27452 bombyx mori	076208 hyphantria	Q8r946 thermoanaer	Q8i8d7 entamoeba h
SOMMERTES	dī	Q27598	90806Q	Q9Y0B3	044249	Q9AW53	QBXI15	Q8ILPS	Q95R43	O9W1V6	Q811F6	O9BLG6	060360	Q27452	076208	Q8R946	Q818D7
	h DB	0 5	0	1 5	S S	• •	9 16	9	3	3	3	G S	3	آع 5	7 5	91 8	1 5
	% Query Match Length DB	069	069	691		144								693			43
	% Query Match	75.4	75.4	75.4	73.7	71.9	71.9	71.9	70.2	70.2	70.2	70.2	70.2	70.2	70.2	68.4	68.4
	Score	43	43	43	42	41	41	41	40	40	40	40	40	40	40	39	39
	Result No.		N	e	4	ĸ	g	7	80	σ	10	11	12	13	14	15	16

Q9rgz5 bacillus ps Q8elv6 oceanobacil Q9wuG6 rattus norv Q8att0 yersinia pe Q97uy7 suffolobus	യമാ	Q8d404 vibrio vuln Q12350 saccharomyc Q72591 beet soil-b	Q99.10 macaz rasc Q98.yi1 homo sapien Q92al0 listeria in Q9598 listeria mo Q9bld9 drosophila Q99521 drosophila	ويوفات	Q96d2rl wiggleswort Q9hpl6 halobacteri Q9cmr9 pasteurella Q9ctr2 mus musculu Q99n31 mus musculu
2 Q9RGZ5 16 Q8ELV6 11 Q9WU06 16 Q8ZDT0 17 Q97UY7	10 49LJA6 5 295V11 5 2816K2 5 29Y0B4 16 P70811	16 Q8D404 3 Q12350 12 O72591	6 Q95JT8 4 Q8WYII 16 Q92ALO 16 Q8Y698 5 Q9BLD9 5 Q9V521	5 Q8WSI5 5 Q44250 5 Q9GVA6 5 Q9GVA5 16 Q8CMW9	16 Q8D2R1 17 Q9HPL6 16 Q9CMR9 11 Q9CTR2 11 Q99N31
805 805 829 446	684 684 684 684 685 684	301	400 406 552 552 670 684	687 688 690 699	153 225 242 243 293
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117 118 20 21	2 2 2 2 2 2 4 4 2 2	222		3 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 4 4 5 6 4 8

## ALIGNMENTS

STRAIN=OREGON-R;
MEDLINE=95372361; PubMed=7644493;
Fujimcto K., Okino N., Kawabata S., Iwanaga S., Ohnishi E.;
Fujimctoc K., Okino N., Kawabata S., Iwanaga S., Ohnishi E.;
"Nuclectide sequence of the cDNA encoding the proenzyme of phenol oxidase Al of Drosophila melanogaster.";
Proc. Natl. Acad. Sci. U.S.A. 92:7769-7773(1995). Drosophila melanogaster (Fruit fly). Bukaryota, Metazoa, Arthropoda; Haxapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1902 (TrEMBLrel. 22, Last annotation update) PRO-phenol oxidase Al (EC 1.14.18.1) (BLACK cells protein). BC OR CG5779. 14 069 14 069 PRT; PRELIMINARY; SEQUENCE FROM N.A. \_TaxID=7227; 027598 RESULT 1 Q27598 

SEQUENCE FROM N.A.

Celniker S.E., Aghavani A., Arcaina T.T., Baxter E., Blazej R.G., Chew M., Doyle C.M., Farfan D.E., Flanagan J., Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim S.H., Lee B., Lomotan M.A., Mazda P., Mok M.S., Moshrefi A.R., Moshrefi M., Nixon K., Pacleb J.M., Park S., Pfeiffer B., Punch D., Snir E., Twomey B., Man K.H., Mittelaw K.R., Zhang R., Zieran L.L., Kimmel B., Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases. STRAIN-BERKELEY;

EMBL; AC004640; -; NOT\_ANNOTATED\_CDS. HSSP; P04253; 1LLA. FlyBase; FBgn000165; Bc.
InterPro; IPR000896; Hemcoyanin.
InterPro; IPR005203; hemcoyanin C.
InterPro; IPR005204; hemcoyanin\_N.

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Q9Y0B3
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adamstides P.G., Scherer S.E., Lib PW., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Champen M., Heiffers B.D.,

RA Brandon R.C., Rogers Y.H.C., Blazed R.G., Champen M., Feliffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basua A., Baxendale J., Bayraktarogulu L., Basaley E.M.,

RA Beson K.Y., Bencos P.V., Bernan B.P., Bhandari D., Bolshakov S.,

RA Beson K.Y., Bencos P.V., Bernan B.P., Bhandari D., Bolshakov S.,

RA Berkova D., Botchen M.R., Bouck J., Bryesterin P., Brottier P.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cavaley S., Dahlke C., Davenport L.B., Davies P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cavaley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Grobics B., Boalcher A., Garg M., Dugan-Rocha S., Pleischmann W.,

RA Glodek A., Gonrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gonrell J.H., Gu Z., Kennison J.A., Ketchum K.A.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Liu X., Mattei B., McIntosh T.C., McLood M.P., Moshrefi A.,

Allasko P., Lei Y., Levitsky A.A., Ill J., Li Z., Liang Y., Ini X.,

RA Liu X., Mattei B., McIntosh T.C., McLood M.P., Parcin V., Reese M.G.,

RA Alazzolo M., Fittman G.S., Pan S., Pollard J., Moshrefi A.,

RA Balazzolo M., Pittman G.S., Pan S., Pollard J., Mang X.,

RA Shire B.C., Siden-Kiander R., Wenter E., Wang A.H., Wang X.,

RA Palazzolo M., Strumer R., Venter E., Wang A.H., Wang X.,

RA Reinett K., Reenington K., Simpson M., Wang X., Wang S., Yao Q.A.,

RA Reinett S., Wassarman D.A., Weinstock G.M., Wang S., Yao Q.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                  5; Length 690;
                                                                                                                                            187 D -> E (IN STRAIN BERKELEY).
505 L -> V (IN STRAIN BERKELEY).
79090 MW; 7F2D6564651B1F58 CRC64;
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                              Score 43; DB 5; Pred. No. 36; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               690 AA
          Pfan, PF00372; hemocyanin, 1.
Pfan, PF03723; hemocyanin_C; 1.
Pfan; PF03722; hemocyanin_N; 1.
PROSTE; PS00187; HAEMOCYANIN 1.
PROSITE; PS00209; HEMOCYANIN 1; 1.
PROSITE; PS00210; HEMOCYANIN 2; 1.
PROSITE; PS06498; TYROSINASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
InterPro; IPR002227; Tyrosinase.
                                                                                                                              Oxidoreductase; Polymorphism.
                                                                                                                                                                                                              75.48;
71.48;
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01-MAY-2000 (TrEMBLrel. 13,
01-0CT-2002 (TrEMBLrel. 22,
BC Gene product (GH04080P).
BC OR CG5779.
                                                                                                                                                                                             Query Match
Best Local Similarity 71.3
Fest Local Si Conservative
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Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Prerygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Oestroidea,
Sarcophagidae, Sarcophaga.
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong R.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                            STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Embitted (COT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR003801, AAE5775.1, --
EMBL, AY060617, AAL28165.1; --
HSSP, P04253, 1LLA.
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Pred. No. 36;
2; Mismatches 0; Indels
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MEDLINE=20359206; PubMed=10899462;
Chase M.R., Raina K., Bruno J., Sugumaran M.;
"Purification, characterization and molecular cloning of prophenoloxidases from Sarcophaga bullata.";
Insect Biochem. Mol. Biol. 30:953-967(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF0372; hemocyanin; 1.
Pfam; PF0372; hemocyanin c; 1.
Pfam; PF0372; hemocyanin n; 1.
PRINTS; PF00187; HAMOCYANIN n; 1.
PROSITE; PS00209; HEMOCYANIN 1; 1.
PROSITE; PS00219; HEMOCYANIN 1; 1.
PROSITE; PS00498; TYROSINASE 2; 1.
SEQUENCE 690 AA; 79090 MW; 49FC131F12D0B893 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
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InterPro; IPR001896; Hemocyanin.
InterPro; IPR005203; hemocyanin.
InterPro; IPR005204; hemocyanin.
InterPro; IPR002227; Tyrosinase.
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InterPro; IPR000896; Hemocyanin.
InterPro; IPR005203; hemocyanin C.
InterPro; IPR005204; hemocyanin N.
InterPro; IPR00504; RNA_rec_mot.
InterPro; IPR02227; Tyrosinase.
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Pfam; PF03723; hemcoyanin_C; 1.
Pfam; PF03723; hemcoyanin_N; 1.
PRINTS; PR00187; HAEMCOYANIN_1:
PROSITE; PS00209; HEMCOYANIN_1: 1.
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71.4%;
                                                                                      Science 287:2185-2195(2000)
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Q9Y0B3;
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Matches
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RESULT 6
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annocation update)
Ubiquitin-conjugating enzyme E2-21 KD (EC 6.3.2.19) (Ubiquitin-protein UCE-E2.
                                                                                                                                                                                        044249;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-1998 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pro-phenol oxidase subunit 1 (EC 1.14.18.1).
Manduca sexta (Tobacco hawkmeth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Dirrysia; Sphinglodea;
                                                                            Gaps
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A Jiang H., Wang Y., Ma C., Kanost M.R.;

Jiang H., Wang Y., Ma C., Kanost M.R.;

Subunit composition of pro-phenol oxidase from Manduca sexta:

T molecular cloning of subunit ProPO-PI.";

I nsect Biochem. Mol. Biol. 27:835-850(1997).

R EMBL; AF00323; AAC05796.1;

R InterPro; IPR000896; Hemccyanin.

R InterPro; IPR005203; hemccyanin.

R InterPro; IPR005203; hemccyanin.

R InterPro; IPR005204; Hemccyanin.

R InterPro; IPR00521; Tyrosinase.

R Pfam; PF0372; hemccyanin.C;

R Pfam; PF03722; hemccyanin.C;

R Pfam; PF03722; hemccyanin.C;

R Pfam; PF03722; hemccyanin.N; 1.
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                                                   75.4%; Score 43; DB 5; Length 691; 71.4%; Pred. No. 36; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
        PROSITE; PS00030; RRM RNP 1; 1.
PROSITE; PS00498; TYRŌSINĀSE 2; 1.
SEQUENCE 691 AA; 79796 MW; DD7545E82CABC94D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            685 AA; 78965 MW; BE5811D145302583 CRC64;
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Eukaryota, Cryptophyta, Cryptomonadaceae; Guillardia.
NCBI_TaxID=55529;
                                                                                                                                                                               685 AA.
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                                                                                                                                                                               PRT;
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PROSITE; PSO02009; HEMOCYANIN 1; 1.
PROSITE; PSO010; HEMOCYANIN 2; 1.
PROSITE; PSO0498; TYROSINASE_2; 1.
 PROSITE; PS00210; HEMOCYANIN 2; 1.
                                                                                                                                                                                                                                                                               Sphingidae, Sphinginae, Manduca.
                                            Query Match
Best Local Similarity 71.4°
'-'hes 5; Conservative
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Best Local Similarity 66...
...nes 6; Conservative
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404 YRWHGFI 410
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MEDLINE-21223349; PubMed=11323671;
A DOUGLAS 5., Zaunar S., Faunholz M., Beaton M., Penny S., Deng L.,
A WEDLINE-21223349; PubMed=11323671;
A WA X., Reith M., Cavaliar-Smith T., Maier U.;
I "The highly reduced genome of an enslaved algal nucleus.";
I wature 4 Aro:1091-1096 (2001).
I PROTEINS (BY SIMILARITY).
I PATHWAY: UBIQUITIN CONJUGATION, SECOND STEP.
I MISCELLANBOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
THIOLESTER FORMATION (BY SIMILARITY).
I PROTEINS (BY SIMIL
SEQUENCE FROM N.A.
MEDLINE=20087226; PubMed=10618395;
Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M.,
Zavaler-Smith T., Maier U., Douglas S.,
"Chloroplast protein and centrosomal genes, a tRNA intron, and odd
telomeres in an unusually compact eukaryotic genome, the cryptomonad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium.
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PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
Ligase; Ubl conjugation pathway.
SEQUENCE 144 AA; 16365 MW; D8D4B2DD6EF74E80 CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002)
BMBL; AP003133; BAB82015.1;
Interpro; IPR001360; Glyco.hydro.1.
Pfan; PP0023; Glyco.hydro.1;
PRINTS; PR00131; GLHYDRLASE1.
ProDom; PD000650; Glyco.hydro.1; 1.
                                                                                                                                                                                                                                                                              nucleomorph.";
Proc. Natl. Acad. Sci. U.S.A. 97:200-205(2000)
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InterPro; 1PR000608; UBQ_conjugat.
Elam; PF00179; UQ_con; 1.
ProDom; PD000461; UBQ_cnjugat; 1.
SMART; SM00212; UBCc; 1.
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Matches 6; Conservative
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PubMed=11792842;
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SEQUENCE 459 AA;
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Beta-glucosidase.
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                   Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF14_0199.
Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata; Apicomplexa, Haemosporida, Plasmodium.
                      71.9%; Score 41; DB 16; Length 459; 100.0%; Pred. No. 52; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 419:498-511(2002).

EMBL, AR014819; ARN36811.1; -.

Hypochetical protein.

SEQUENCE 1149 AA; 137812 MW; 5C3B42A34DCCBFCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pred. No. 1.3e+02;
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66.7%;
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
Query Match
Best Local Similarity luve.
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Adding N. J. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adding M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adding M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Adding S.E., Sichards S., Ashburner M., Henderson S.N., Batton G.G., Wortman J.T., Yandell M.D., Zhang O., Chen L.X., Brand O. Chen L.X., Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D., Bratton G.G., Wortman J.T., Andrews-Pfannkoch C., Baldwin D., RA Brandon R.C., Rogers Y. H.C., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Rallew R.M., Bauu A., Baxendalbe J., Bayraktaroglu L., Beasley E.M., Ranns R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Borters K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Acklery J. M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Berraz C., Ferriara S., Ferischmann W., Roslon K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Brangelista C.C., Ferraz C., Ferriara S., Ferischmann K.A. Godbriellan R.E., Garra N.S., Gelbart W.M., Glasser K., Hostin D., Houston K.A., Howland T.J., Hernandez J.S., Horris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.S., Murph D., Lin Z., Liang Y., Lin X., Roslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegvam C., Alalin M., Kalush F., Karpen G.H., Ke Z., Kennison D.A., Kattel B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Lia Z., Liang Y., Lin X., Murph B., Mattel B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Lia Z., Liang Y., Lin X., Murch S., Murph B., Murlhov G., Milshina N.V., Mobarry C., Morese M.G., Siden-Kiamos B., Nelson D.E., Radies D. B., Nelson D.E., Radies D. S., Pollard J., Pull J., Pull J., Pull J., Radies D., Shen K., Suber M., Wang A., Wang S., Pollard J., Pull J., Radies D., Shen K., Siden-K., Shen H., Wang S., Pollard J., 
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                         Score 40; DB 5; Length 683;
Pred. No. 1.1e+02;
1; Mismatches 1; Indels
                                                                                      Pfam; PF00372; hemocyanin; 1.
Pfam; PF03723; hemocyanin, C; 1.
PFam; PF03722; hemocyanin, N; 1.
PFINITS; PR00120; hEMOCYANIN, 1.
PROSITE; PS00209; HEMOCYANIN, 1; 1.
PROSITE; PS00210; HEMOCYANIN, 2; 1.
PROSITE; PS00498; TYROSINASE_2; 1.
SROUGNCE 683 AA; 79251 MW; E0E3F7E32E40F20B CRC64;
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Last annotation update)
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01-MMY-2000 (TrEMBLrel. 13, Created)
01-MMY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
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InterPro, IPR00896, Hemocyanin.
InterPro, IPR005203, hemocyanin.
InterPro, IPR005204, hemocyanin.
InterPro, IPR002227; Tyrosinase.
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5; Conservative
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403 YKWHAFI 409
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STRAIN=a80;
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Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2195(2000).

Science 287:2195(2000).

EMBL, AE003459; AAF46946.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Tucson 14021-0224.0;
MEDLINE=22426072; PubMed=12537575;
Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins R.A.,
Gnirke A., Mungall C.G., Wang A.M., Krommiller B., Pacleb J., Park S.,
Stapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G.M.,
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EMBL; AY190941; AAOO1013.1; -. SEQUENCE 683 AA; 79054 MW; 9FF9A0E2A970662A CRC64;
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                                                                                                                                                                                                                                                             Length 683;
                                                                                          HIST: PG-253; 10AT.

FIRST: PG-253; 10AT.

InterPro; IPR0000497; Dox-A3.

InterPro; IPR005204; Hemocyanin.

InterPro; IPR005204; Hemocyanin.

InterPro; IPR005227; Tyrosinase.

Ffam; PF00372; hemocyanin.; 1.

Pfam; PF03722; hemocyanin. 7: 1.

Pfam; PR03722; hemocyanin. N: 1.

R PROSITE; PS00209; HEMOCYANIN. 1; 1.

R PROSITE; PS00209; HEMOCYANIN. 2: 1.

R PROSITE; PS002498; TYROSINASE 2: 1.

S PROSITE; PS002498; TYROSINASE 2: 1.

S PROSITE; PS002498; TYROSINASE 2: 1.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                             70.2%; Score 40; DB 5; I 71.4%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                          683 AA.
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01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila erecta (Fruit fly).
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Best Local Similarity 71...
S; Conservative
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Best Local Similarity
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Cuticular pro-phenoloxidase of the silkworm, Bombyx mori.

Purification and demonstration of its transport from hemolymph.";

J. Biol. Chem. 276:11100-11112(2001).

J. Biol. Chem. 276:11100-11112(2001).

HSSP, P04253; 10XY.

InterPro; IPR000896; Hemocyanin.

InterPro; IPR005203; hemocyanin.

InterPro; IPR005203; hemocyanin.

InterPro; IPR005227; Tyrosinase.
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF178461; AAG09303.1; -.
HSSP; P04253; 10XY.
InterPro; IPR005203; Hemocyanin.
InterPro; IPR005204; hemocyanin.
InterPro; IPR005204; hemocyanin. N.
InterPro; IPR005207; Tyrosinase.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Prophenoloxidase-2 (EC 1.14.18.1).
01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-WAR-2003 (TrEMBLrel. 23, Last annotation update) Prophenoloxidase-2s. Bombya mori (Silk moth).
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MEDLINE=21179161; PubMed=11118441;
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Pfam; PF0372; hemocyanin_C; 1.
Pfam; PF0372; hemocyanin_N; 1.
PRINTS; PR00187; HARNCYANIN_1.
PROSITE; P500210; HEMOCYANIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE, PS00209; HEMOCYANIN 1; 1. PROSITE; PS00210; HEMOCYANIN 2; 1. PROSITE; PS00498; TYROSINAS; 2; 1. SEQUENCE 693 AA; B0181 MW; 3A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00372; hemocyanin; 1.
Pfam; PF03723; hemocyanin, C; 1.
Pfam; PF03722; hemocyanin_N; 1.
PRINTS; PR00187; HAEMOCYANIN.
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Best Local Similarity 44.*.
Gest A; Conservative
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Query Match
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
NCBI_TaxID=7091;
                                                                                                                             Gaps
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STRAIN=KINBRIN X SHOWA; TISSUE=Hemocyte;
STRAIN=KINBRIN X SHOWA; TISSUE=Hemocyte;
Kawabata T., Yasuhara Y., Ochiai M., Matsuura S., Ashida M.;
"Molf-cular clohing of insect pro-phenol oxidase: a copper-containing protein homologous to arthropod hemocyanin.";
Proc. Natl. Acad. Sci. U.S.A. 92:7774-7778(1995).
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01-07AN-1999 (TrEMBLrel. 09, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
PROPHENOLOXIDASE subunit 2 (EC 1.14.18.1) (PROPHENOLOXIDASE-2F).
Bombyx mori (Silk moth).
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                                                                             Match 70.2%; Score 40; DB 5; Length 693; Local Similarity 44.4%; Pred. No. 1.1e+02; tes 4; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asano T., Ashida M.;
Asano T., Ashida M.;
"Pro-phenoloxidase type-2(f) 2.3 kbp Bombyx mori.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; D49371, BAA08369.1; -.
EMBL; AB048762; BAB41101.1; -.
                      Oxidoreductase.
SEQUENCE 693 AA; 79994 MW; FD71A7593A9312EB CRC64;
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InterPro; IPR000896; Hemocyanin.
InterPro; IPR005203; hemocyanin.
InterPro; IPR005204; hemocyanin.C.
InterPro; IPR005207; Tyrosinase.
Pfam; PP00372; hemocyanin; 1.
Pfam; PP03722; hemocyanin; 1.
Pfam; PP03722; hemocyanin, C; 1.
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PROSTIE: PS00209; HEMOCYANIN 1; 1.
PROSITE; PS00210; HEMOCYANIN 2; 1.
PROSITE; PS00498; TYROSINASE_2; 1.
PROSITE; PS00498; TYROSINASE_2; 1.
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Best Local Similarity 44.4%;
Matches 4; Conservative
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Matches
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Hyphantria cunea (Fall webworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Arctiidae; Hyphantria.
NCBI_TaxID=39466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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MEDLINE-1991336;
MEDLINE-199136.
BAO Q. Tian Y. Li W. Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98199915; PubMed=9537761;
Park D.S., Shin S.W., Kim M.G., Park S.S., Lee W.J., Brey P.T.,
Park H.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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"Isolation and characterization of the cDNA encoding the prophenoloxidase of fall webworm, hyphantria cunea.";

Insect Blochem. Mol. Biol. 27:983-992(1997).

E BMBL, AFC02031; AAC34256.1; ...

R H5SP, P04253; 10XY.

R InterPro; IPR00896; Hemocyanin.

R InterPro; IPR005201; hemocyanin.

R InterPro; IPR005201; hemocyanin.

R Pfam; PF03723; hemocyanin. 1; 1.

R Pfam; PF03723; hemocyanin. 2; 1.

R PRINTS; PR00129; HEMOCYANIN.

R PRINTS; PR00129; HEMOCYANIN.

R PROSITE; PS00209; HEMOCYANIN. 2; 1.

R PROSITE; PS00209; HEMOCYANIN. 2; 1.

R PROSITE; PS00499; TYROSINASE. 2; 1.

R PROSITE; PS00499; TYROSINASE. 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.2%; Score 40; DB 5; Length 697; Best Local Similarity 44.4%; Pred. No. 1.2e+02; Matches 4; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 AA; 31031 MW; FDF3A13D14FDCFEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBR946;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Pseudouridylate synthase, 238 RNA-specific.
RLUA2 OR TTE1780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 AA.
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INTERPROJ. IPRO06145; PseudoU synth.
INTERPRO; IPRO06225; Pseud RIUD.
INTERPRO; IPRO06224; PSI RIU.
Pfam; PF00849; PseudoU synth 2; 1.
ProDom; PD001819; PSI RIU; 1.
TIGRRAMS; TIGR00005; rluD subfam; 1.
PROSITE; PS01129; PSI_RIU; 1.
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SEQUENCE 268 AA
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6

0; Gaps

Matches 5; Conservative 1; Mismatches 0; Indels

Qy 2 LYKWHG 7
: | | | | | |
Db 13 MYKWHG 18

Search completed: December 16, 2003, 14:17:57
Job time: 27 secs

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December 16, 2003, 14:06:05; Search time 33 Seconds (without alignments) 43.289 Million cell updates/sec
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2: /SIDSI/godata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/godata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDSI/godata/geneseq/geneseqp-embl/AA1982.DAT:*
5: /SIDSI/godata/geneseq/geneseqp-embl/AA1984.DAT:*
5: /SIDSI/godata/geneseq/geneseqp-embl/AA1986.DAT:*
7: /SIDSI/godata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDSI/godata/geneseq/geneseqp-embl/AA1980.DAT:*
9: /SIDSI/godata/geneseq/geneseqp-embl/AA1980.DAT:*
10: /SIDSI/godata/geneseq/geneseqp-embl/AA1980.DAT:*
11: /SIDSI/godata/geneseq/geneseqp-embl/AA1991.DAT:*
12: /SIDSI/godata/geneseq/geneseqp-embl/AA1992.DAT:*
13: /SIDSI/godata/geneseq/geneseqp-embl/AA1993.DAT:*
14: /SIDSI/godata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDSI/godata/geneseq/geneseqp-embl/AA1993.DAT:*
16: /SIDSI/godata/geneseq/geneseqp-embl/AA1993.DAT:*
17: /SIDSI/godata/geneseq/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/godata/geneseq/geneseqp-embl/AA1995.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITAMADITEC

			Description	Human cancer antio	C qlutamicum prote	Human cancer antiq	Human cancer antig	Drosophila melanog	Human protein SEO	Human prostate can	Human ORFX protein	N-terminal fragmen
SUMMAKTES			_	TAU7#682	CHG92893	AAU74685 .	AAU74684	ABB63728	ABP64908	AB56395	ABP00720	AAR57000
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N-terminal fragmen Zea mays protein f Zea mays protein f Zea mays protein f Zea mays protein f Partial sequence o	ug metabo cod gp. A transfera cod group cod group	blood of trans brans brans brans blood of blood of trans	e e pere e a a a a a a a a a a a a a a a a a	Helicobacter pylor Helicobacter pylor Helicobacter pylor Human topoisomeras Helicobacter pylor Helicobacter pylor Helicobacter pylor Helicobacter pylor
054040	AAE05193 AAR11317 AAR57011 AAC29231 AAO21510 AAR11789	AAR11792 AAR57013 AAR57016 AAR57020 AAR29232 AA021511	AAR 7021 AAM 4218 AAA 6423 AAA 26506 ABU51459 ABU51593 ABU52086	ABUS1112 ABUS1190 ABUS1190 AAO26505 ABUS1873 ABUS12204 ABUS1676
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## ALIGNMENTS

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Human, cancer antigen; ATF4; CRBB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC, major histocompatibility complex; adoptive immunotherapy; cancer; overian cancer.
                                                                                   Human cancer antigen ATF4/CREB-2 based immunogenic ligand #2
                      AAU74682 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                           31-MAY-2000; 2000US-209388P. 20-DEC-2000; 2000US-257007P.
                                                                                                                                                                                                                       30-MAY-2001; 2001WO-US17454.
                                                              (first entry)
                                                                                                                                                                                                                                                                         (GENZ ) GENZYME CORP.
                                                                                                                                                                                                                                                                                                                   WPI; 2002-097764/13.
                                                                                                                                                                          WO200192306-AŽ.
                                                                                                                                                                                                                                                                                               Nicolette CA;
                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                  06-DEC-2001.
                                                              09-APR-2002
                                                                                                                                                           Synthetic.
                                          AAU74682;
RESULT 1
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer articles ATF4/CREB-2. Gnot defined) and the polynucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising the compound, a method of immunotherapy comprising administering to a subject the antibody, an immuno effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antibod presenting coll that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune especially useful in gene therapy or as compounds. The compounds are useful for reating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for reating cancer, particularly coaring cancer. The compounds are useful for reating cancer, particularly coaring cancer. The compounds are useful for reating cancer, particularly coaring cancer. The compounds are also useful for generating antibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polynuclectides are useful in diagnostic methods, for the detection and purification of antibodies, or as immunogenic a human cancer antigen Aff4/CREB-2 based immunogenic compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respectively but have not been cross-referenced or CDS features put in due to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
New therapeutic compounds comprising immunogenic ligands, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yokoi H;
                      modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 52; DB 23; 100.0%; Pred. No. 9.3e+05; ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG92893 standard; Protein; 1043 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degeneracy of the DNA sequences.
                                                                                 Claim 2; Page 55; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0377484.
2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2000; 2000EP-0127688.
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Best Local Similarity
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03-AUG-2000;
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The present invention provides a number of nucleotide and protein agequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, coryneform bacterium, Coryneform bacterium, Coryneform bacterium, coryneform bacterium, patterifying a homologue of a gene derived from coryneform bacterium, coryneform bacterium, patterifying a numbor acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, cancer antigen, ATF4; CREB-2; vaccine, cytostatic,
immunogenic ligand, gene therapy; MHC; major histocompatibility complex;
adoptive immunotherapy; cancer; ovarian cancer.
                                                                                Novel polymucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                             Claim 17; SEQ ID NO: 6647; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.7%; Score 43; DB 22; Length 1043; 77.8%; Pred. No. 27; ive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cancer antigen ATF4/CREB-2 based immunogenic ligand #5.
rateishi N, Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU74685 standard; Peptide; 9 AA
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20-DEC-2000; 2000US-257007P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 FLHSAHFYV 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FLHKVHFYV 9
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                                    MPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1043 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                     N-PSDB; AAH68112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200192306-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigion ATP4/CREB-2. (not defined) and the polymucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method of immunotherapy comprising the compound, a method of immunotherapy comprising the compound, a method of immunotherapy comprising dealivering the compound, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antisping presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response of context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response of the synthetic and naturally occurring compounds. The compounds are useful for medulating an immune response to the synthetic and naturally or as components of antibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polyfication of antibodies, or as immunogens for the detection and purification of antibodies, or as immunogens for the production of antibodies. The invantion of the invantion of antibodies. The invantion of the invantion of antibodies are immunogenic companies. The invantion and purification of antibodies, or sequence represents a human cancer antigen ATF4/CRB-2 based immunogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, cancer antigen, ATF4; CRBB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respective. but have not been cross-referenced or CDS features put in due to the degeneracy of the DNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cancer antigen ATF4/CREB-2 based immunogenic ligand #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.8%; Score 41; DB 23; Length 9; 77.8%; Pred. No. 9.3e+05; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU74684 standard; Peptide; 9 AA.
Claim 5; Page 56; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2001; 2001WO-US17454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-2000; 2000US-209388P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-2000; 2000US-257007P
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200192306-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicolette CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigien ATP4/CREB-2 foot defined) and the polymuclectides encoding them. Also included are an antibody that specifically recognises and binds them. CC compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising computing computation or in vivo in the presence and at the expense of an antistering to a subject the air intrody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antistering or presenting cell that presents the immunogenic compound a method of adoptive immunotherapy comprising administering the immune response context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response cc the synthetic and naturally occurring compounds. The compounds are useful for modulating an immune response to the synthetic and naturally or as components of anti-cancer vectimes. The compounds are useful for treating cancer, particularly recognise and bind to these molecules. These antibodies are further useful for immunotherapy when administered to a castimenosens for the production and purification of antibodies, or as immunogens for the production of antibodies. The present correct in the present antigen ATF4/CREB-2 based immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respectively but have not been cross-referenced or CDS features put in due to the degeneracy of the DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
New therapeutic compounds comprising immunogenic ligands, useful for
                      for treating ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
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o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 17976.
                   modulating an immune response, particularly for t cancer, and as components of anticancer vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB63728 standard; Protein; 979 AA.
                                                                                 Claim 4; Page 56; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ligand of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
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hammetopoletic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; nootropic; antial[ammateoxy; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide;
                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity -
                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                           insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                        Disclosure; SEQ ID NO 17976; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 39; DB 22; Length 979; 85.7%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP64908 standard; Protein; 1044 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunostimulant; cerebroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-NOV-2001; 2001WO-US42950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000; 2000US-0714936
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WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                  (ABB57737-ABB72072)
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      979 AA;
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                    N-PSDB; ABL07831
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                                                                                        interactions -
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The present invention relates to novel human coding sequences

(ABQ99568-ABQ99608) and proteins (ABP64682-ABP65022). The sequences are

cueful in therapeutic, diagnostic and research methods. The

polynucleotides may be used in the field of molecular biology as

hybridisation probes, primers for PCR, for chromosome and gene mapping,

control of production of protein, or in generation of anti-sense

the recombinant production of protein, or in generation of anti-sense

the polynucleotides are useful in diagnostics as expressed

sequence tags (ESTs) for identifying expressed genes or for physical

mapping of the human genome. The proteins may be used as molecular weight

control of maintain and expand cell population in a totipotential or

puripotential state useful for re-engineering damaged or diseased

tissues, transplantation, manufacture of bio-pharmaceuticals or the

cused to maintain and expand cell population in a totipotential or

puripotential state useful for re-engineering damaged or diseased

tissues, transplantation, manufacture of bio-pharmaceuticals or the

cused to maintain or biological activity, e.g. haematopoietic disorders,

for preventing, treating or ameliorating disorders involving aberrant

contral/peripheral nervous system diseases, mechanical and traumatic

disorders, non-healing wounds, immune descinencies and disorders,

cuted from ESTs isolated mainly by sequencing by hybridisation, and

disorders, or cancer. The polynucleotide sequences of the invention were

assembled from ESTs isolated mainly by sequencing by hybridisation, and

cassembled from ESTs isolated mainly by sequencing by hybridisation, and

in some cases, sequences obtained from one or more public databases.

Note: The sequence data for this patent did not form part of the printed

specification, but was obtained in electronic format directly from Wipo, at ftp.wipo.int/pub/published_pot_esquences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, prostate cancer, prostate cancer antigen, detection, diagnosis, neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological, antibacterial, gene therapy, neural, immune, reproductive, renal, gastrointestinal, pulmonary, cardiovascular, proliferative disorder, wound, infectious disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate cancer antigen protein sequence SEQ ID NO:973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%; Score 39; DB 23; Length 1044; 75.0%; Pred. No. 1.4e+02; tive 1; Mismatches 1; Indels 0
Claim 20; SEQ ID 568; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB56395 standard; Protein; 102 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38-MAR-2000; 2000WO-US05988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-2001 (first entry)
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hes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1044 AA;
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(CURA-) CURAGEN CORP. WPI; 2002-106308/14. Query Match Best Local Similarity myasthenia gravis. N-PSDB; ABN16472. N-PSDB; AAF15598. WO200192523-A2. Shimkets RA, Homo sapiens. 24-JUN-2002 06-DEC-2001. invention. Sequence ABP00720; Matches RESULT 8
ABPO0720
XX
ARPO0720
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ARPO
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DIT 24-J
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DIT 27-J
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AAR57000 standard; peptide; 25 AA.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 FINSIHIYI 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
15-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5326857-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR57000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                         APPLISSON O AMPLISSON CALCAGE LINE AND APPLISSON CAUGES ASSOCIATED PROTECTION. CALLED PROSTAGE CANDER AND APPLISSON CALLED PROSTAGE CANDER AND APPLICATION.

The prostage cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, valneary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polymucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAPIGSOR to AAPIGS1 to AABS7303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhange; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                  Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                               AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.1%; Score 38; DB 21; Length 102; 75.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ORFX protein sequence SEQ ID NO:1422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                           Claim 11; Page 1413; 2338pp; English.
                                                                    disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP00720 standard; Protein; 79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||:|||
4 FEHKLHFY 11
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The present invertion userings substantially putities. The present invertion userings substantially putities.

(Teferred to as open reading frame, ORFX, where X is 1-11491 process.)

In the specification). ABN15/62 to ABN27252 encode the human ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynuclectide can be used in gene therapy. ORFX sequences can be used in the therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, consciously and the organization of cancer, hyperproliferative disorders, cirrhosis of liver, contentration, cardiovascular diseases, disorders related to organization, cardiovascular diseases, disorders related to organizations preventation, cardiovascular diseases, disorders related to organization, cardiovascular diseases, disorders, infectious disease, autoimmune disorders such as multiple sclerosis, infectious disease, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, consequence data for disorders, incisions, ulcers, for treating osteoporosis, conception or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from consecution, but was obtained in electronic format directly from WIPO configuration, but was obtained in electronic format directly from WIPO configuration, but was obtained in electronic format directly from WIPO configuration, but was obtained in electronic format directly from WIPO configuration.
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                                                                                                                                                                                                              The present invention describes substantially purified human proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.2%; Score 37; DB 23; Length 79; 44.4%; Pred. No. 23; ive 3; Mismatches 2; Indels
hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Unsure.
/note= "This amino acid is unknown."
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/note= "This amino acid is unknown."
                                                                                                            Disclosure, SEQ ID 1422; 1037pp; English.
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89US-0402695

31-AUG-1989;

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06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
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23-APR-1999;
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29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-APR-1999
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                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                   AAG12473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blood, group, determinant; antigen; erythrocyte; oligosaccharide; glycoconjugate; glycosphingolipid; glycoprotein; glycosyltransferase;
                                                                                                                             The histo-blood group ABH determinants are major allogeneic antigens in both erythrocytes and tissues of humans. They generally constitute peripheral parts of the oligosaccharide chains of glycoconjugates i.e.linked to lipids (glycosphingolipids) or to proteins (glycoproteins). It was proposed that the A and B phenotypes were associated with glycosyltransferases that converted the H substance associated with the O phenotype to A and B respectively, through the addition of alphal-3-N-acetylgalactosamine or alphal-3-galactosyl residues to the H antigen Fuc-alphal-2Gal-betal-R. Hence, the primary products of the histo-blood group A and B genes are the respectively glycosyltransferases. This is a firagment of the A group transferase. This is a (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated DNA molecules - encode human histo-blood groups A-, B- and O-glycotransferases
                                                                              å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-terminal fragment of human histo-blood group A transferase.
                                                                             Isolated DNA molecules - encode human histo-blood groups A-,
                                                                                                                                                                                                                                                                                           69.2%; Score 36; DB 15; Length 25; 71.4%; Pred. No. 11; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clausen H, Hakomori S, White T, Yamamoto F;
                                      White T, Yamamoto F;
                                                                                                           Example 2; Column 35-36; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          AAR57007 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0752101.
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91US-0752101
                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-FEE-1995 (first entry)
                                                                                                                                                                                                                                                                                                     Local Similarity 71.4
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                    (BIOM-) BIOMEMBRANE INST
                                         Hakomori S,
                                                                                         and O-glycotransferases
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
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6 HRVHYYV 12
                                                          WPI; 1994-217098/26
                                                                                                                                                                                                                                                                                                                                    3 HKVHFYV 9
                                                                                                                                                                                                                                                                          25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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 29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-1994.
                                         Clausen H,
                                                                                                                                                                                                                                                                                                                                                                                                                              AAR57007;
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                The histo-blood group ABH determinants are major allogeneic antigens in both erythrocytes and tissues of humans. They generally constitute peripheral parts of the oligosaccharide chains of glycoconjugates i.e.linked to lipids (glycosphingolipids) or to proteins (glycoproteins). It was proposed that the A and B peroteins (glycoproteins). It was proposed that the A and B phenotypes were associated with the O phenotype to A and B converted the substance associated with the O phenotype to A and B converted or alphal-3-galactosyl residues to the H antigen Fuc-alphal-2Gal-betal-R. Hence, the primary products of the histo-blood group A and B genes are the respective glycosyltransferases. This is a largement of the A group transferase. See also AARS6995-R57010. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Example 2; Column 41-42; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG12473 standard; Protein; 95 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37 AA;
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Mismatches
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74 FVHDLHFFV 82
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uus-0137724 uus-0138094 uus-0138847 uus-0139119 uus-0139452 uus-0139453 uus-0139455 uus-0139456 uus-0139456 uus-0139456 uus-0139456 uus-0139456 uus-0139456	990S-0139461. 990S-0139462. 990S-0139463. 990S-0139763. 990S-013989. 990S-0140893. 990S-0140893. 990S-014082. 990S-014287. 990S-014287. 990S-014287. 990S-014287. 990S-014287. 990S-014383. 990S-014433.	90S-0144352 90S-01448632 90S-01448634 90S-0145086 90S-0145086 90S-0145085 90S-0145085 90S-0145185 90S-0145185 90S-0145185 90S-0145185 90S-0145185 90S-0145918 90S-0145918 90S-0146386 90S-0146386 90S-0146386 90S-0146386 90S-0146386 90S-0147304 90S-0147304
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Query Match 69.2%; Score 36; DB 21; Length 166; Best Local Similarity 55.6%; Pred. No. 72; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps

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15-JUL-1999;
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18-JUN-
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Procein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                      Zea mays protein fragment SEQ ID NO: 43259.
                                                                                                         AAG35416 standard; Protein; 182 AA
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990S-0130510.
990S-0131449.
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FVHDLHFFV 120
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AAG 35416

AAG 35416

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AAG 36416

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Blood, group, determinant, antigen; erythrocyte, oligosaccharide; glycoconjugate; glycosphingolipid; glycoprotein; glycosyltransferase; transferase.

Partial sequence of human A transferase

(updated)
(first entry)

25-MAR-2003 16-PEB-1995

AAR57024;

AAR57024 standard; Protein; 195 AA.

/note= "Site of deletion."

US5326857-A

Region

Location/Qualifiers

Homo sapiens

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AAR57024
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Pred. No. 79;
3; Mismatches 1; Indels
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Best Local Similarity
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28-OCT-1999;
29-OCT-1999;
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26-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Clausen H, Hakomori S, White T, Yamamoto F;
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Job time : 33 secs
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20 HRVHYYV 26
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29-AUG-1991;
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RESULT 1
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                                                                                                                          (without alignments)
30.875 Million cell updates/sec
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                                                                                                     December 16, 2003, 14:11:00 ; Search time 12.3333 Seconds
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Sequence 38,
Sequence 39,
Sequence 51,
Sequence 51,
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Sequence 6,
Sequence 6,
Sequence 8,
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-07-752-101A-38
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US-07-752-101A-61
US-08-202-05-6
US-08-802-67A-6
US-08-802-478-6
US-08-801-228-6
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US-09-100-851-1
US-09-265-294-1
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Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 10
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Sequence 6, Appli	Sequence 18, Appl	Sequence 5000, Ap	Sequence 4, Appli	Sequence 2, Appli	~	Sequence 4499, Ap	Sequence 5382, Ap	Sequence 14, Appl	Sequence 24497, A	Sequence 313, App	Sequence 313, App	Sequence 7, Appli	Sequence 48, Appl	Sequence 48, Appl	Sequence 48, Appl	Sequence 671, App	Sequence 4203, Ap
US-08-982-493-6	US-09-322-478-18	US-09-134-001C-5000	US-08-696-139-4	US-08-696-139-2	US-07-698-926A-2	US-09-107-532A-4499	US-09-107-532A-5382	US-08-926-842B-14	US-09-252-991A-24497	US-09-620-412C-313	US-09-598-419-313	US-09-215-694-7	US-09-186-276B-48	US-08-842-445-48	US-09-186-188B-48	US-09-198-452A-671	US-09-134-001C-4203
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374	1802	190	306	404	432	682	191	229	345	691	691	1068	134	134	134	93	166
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65	65	63	63.5	63	63	63	61	61	61	61	61	61	9	9	9	59.6	53
34	34	33	33	33	33	33	32	32	32	32	32	32	31.5	31.5	31.5	31	31
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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US-07-752-101A-6
Sequence 6, Application US/07752101A
Sequence 6, Application US/07752101A
Sequence 6, Application US/07752101A
Sequence 6, Application US/07752101A
Sequence 10.00
SAPELICANT: White, Thayar
APPLICANT: White, Thayar
APPLICANT: Hakowori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES. 69
CORRESPONDENCES. 169
CONTYN: U.S.
TREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
CONTYN: U.S.
THE SEATHS SYSTEM: PC-DOS/NM-DOS
SOUTHER READALE FORM:
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATION
SETTING SYSTEM: PC-DOS/NM-DOS
SOUTHART APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION WINNER: 32.629
REGISTRATION WINNER: 32.629
REGISTRATION WINNER: 32.629
TELECOMMUTICATION INFORMATION:
TELEFRAX: 206-682-6031
TELEFRAX: 206-682-6031
TELEFRAX: 206-682-6031
TELEFRAX: 206-682-6031
TELEFRAX: 1788: PRINCIPLES: SINGLE
TYPE: AMINO ACID
STRANDENSES: single
TYPE: AMINO ACID
STRANDENSES: single
MOLECULE TYPE: Peptide
HYDORIGHTER: Noterminal
FRAMER: RESIDENTION: //Label= unsure
OTHER INFORMATION: //ncce= "These amino acids are unknown".
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us-09-870-089b-5.rai

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                               Query Match 69.2%; Score 36; DB 1; Length 25; Best Local Similarity 71.4%; Pred. No. 4.9; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle
STATE: Washington
COUNTRY: U.S.
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DAME:
CLASSIFICATION:
ATCASSIFICATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32 629
REFERENCE TOOKET NUMBER: 150036.406C1
TELEPHONE: 206-622-4900
TELEPHONE: 206-682-6031
TELEFAX: 3723836
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                             Sequence 13, Application US/07752101A
Patent No. 5226857
GENERAL INFORMATION:
APPLICANT: Yamamoco, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakemori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-07-752-101A-68
IS-07-752-101A-68
Sequence 68, Application US/07752101A
Patent No. 5326857
GENERAL INFORMATION:
APPLICANT: Yamamoto, Fumi-ichiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 71.4:
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 37 amino acid
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                  |:||:||
6 HRVHYYV 12
                                                                                                                          3 HKVHFYV 9
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3 HRVHYYV 9
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US-07-752-101A-13
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US-07-752-101A-6
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                           ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 150036.406C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADORESS:
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBR OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 35, Application US/07752101A ; Patent No. 5326857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 195 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-07-752-101A-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: U.S.
                                                                                                                                             STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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GENERAL INFORMATION:
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                                                                                                                                                                                                          COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-07-752-101A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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Sequence 38, Application US/07752101A Patent No. 5326857 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 15003
TELECOMMUNICATION INFORMATION:
TELEFONE: 206-622-4900
TELEFAX: 206-682-6031
TELEFAX: 3723836
INFORMATION FOR ESO ID NO: 38: 5EQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: MAINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
; FRAGMENT TYPE: N-terminal US-07-752-101A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
COUNTRY: U.S.
ZIP: 98104
                                                                                                                                                                        |:||:||
144 HRVHYYV 150
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145 HRVHYYV 151
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                                                                                                                                                 3 HKVHFYV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                      US-07-752-101A-38
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                                                                                                                                                                                                                                                     RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 150036.406C1
TELECOMMUNICATION INFORMATION:
TELEFRANE: 206-622-4900
TELEFRANE: 206-682-6031
TELEFRA: 3723836
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 150036.406C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEPAX: 206-682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36, Application US/07752101A
Fatent NO. 5336857
GENERAL INFORMATION:
APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19910829
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 3723836
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 353 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 71.4.

Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                               ; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-752-101A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98104
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US-07-752-101A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Wa
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Query Match 69.2%; Score 36; DB 1; Length 353; Best Local Similarity 71.4%; Pred. No. 60; Matches 5; Conservative 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yamamoco, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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; Sequence 39, Application US/07752101A
; Patent No. 5326857
; GENERAL INFORMATION:
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SOFTWARE: Patentin Release #1.0, Version #1.25
         CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWER:
US/07/752,101A
FILING DATE: 19910829
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 150036.406C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEPHONE: 206-622-4900
TELEPHONE: 206-622-4900
TELEPHONE: 3723336
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TTELET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 150036.406C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEPHONE: 206-622-4900
TELEPEX: 3723836
INFORMATION FOR SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 354 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                sss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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145 HRVHYYV 151
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                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-752-101A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-07-752-101A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
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69.2%; Score 36; DB 1; Length 354;
Best Local Similarity 71.4%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                         ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRAITON NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 150036.406C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 266-622-4900
TELEPHONE: 266-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41, Application US/07752101A
Fatent No. 5326857
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wanamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakemori, Sen-itiroh
APPLICANT: Clausen, Henrik
ITTLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CONFRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO FRAGMENT TYPE: N-terminal US-07-752-101A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                              STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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US-07-752-101A-41
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                                                                                                                                                                                                                                                   COUNTRY:
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Query Match 69.2%; Score 36; DB 1; Length 354; Best Local Similarity 71.4%; Pred. No. 60; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                Sequence 51, Application US/07752101A
Patent No. 5326857
GENERAL INFORMATION:
APPLICANT: Yamamoto, Fumi-ichiro
APPLICANT: White, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPRIATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION: 435
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Datin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/202,056 FILING DATE: 25-FEB-1994 CLASSIFICATION ATA: APPLICATION NUMBER: 07/67211 ATTORNEY: APPLICATION NUMBER: 07/67211 ATTORNEY AGENT INFORMATION: NAME: LOVE, RICHARD B. NAME: LOVE, RICHARD B. NAME: LOVE, RICHARD B. REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IELEKA: 910/371-7168
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85./",
Ass 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 415/225-5530
415/952-9881
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128 LHKVNFY 134
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/note= "These amino acids are unknown."
                                                                                                                                                                    69.2%; Score 36; DB 1; Length 354; 71.4%; Pred. No. 60; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 1; Length 375;
Pred. No. 64;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-07-752-101A-52
i Sequence 52, Application US/07752101A
i Patent No. 532687
i GENERAL INFORMATION:
APPLICANT: Mamamoto, Fumi-ichiro
APPLICANT: Mhite, Thayer
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: Hakomori, Sen-itiroh
APPLICANT: APPLICANT: Glausen, Henrik
i APPLICANT: APBRESS:
APPLICANT: Gausen, Henrik
i TITLE OF INVERTION: ABO GENOTYPING
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSES: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REGISTRATION NUMBER: 32,629
REBRENCE/DOCKET NUMBER: 150036.406C1
TELECOMMUNICATION INFORMATION:
TELEPAK: 206-622-4900
TELEFAK: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 372336
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 69.2%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                           HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal
                                                                                                                                                                                             Best Local Similarity 71.4 Matches 5; Conservative
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TOPOLOGY: linear
             TOPOLOGY: Linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
STRANDEDNESS: single
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COCATION: 1..53

OTHER INFORMATION:

OTHER INFORMATION:

US-07-752-101A-52
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STATE: Washington
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145 HRVHYYV 151
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                                                                                                                ; FRAGMENT TYPE
US-07-752-101A-51
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                                                                                                                                                                      Query Match
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0; Gaps
RESULT 11
US-08-202-056-5
; Sequence 5, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Hebert, Caroline
; APPLICANT: Lee, James
; TITE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genethech, Inc.
; STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
CITY: South San Francisco
COUNTRY: USA
ZIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08076093A,
Patent No. 5543503
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Hebert, Caroline
APPLICANT: Hebert, Antibodies to Human PF4A Receptors
UNMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 35; DB 1; Length 372; 85.7%; Pred. No. 94;
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us-09-870-089b-5.rai

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APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA: 1-20-
APPLICATION NUMBER: 07/677211
FILING DATE: 29-WAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08284586
Patent No. 5840856
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85./*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc)
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US-08-284-586-6
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67.3%; Score 35; DB 1; Length 372;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Churcharapai, Anan
APPLICANT: Lee, James
APPLICANT: Lee, James
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Attibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS(MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A FILING DATE: 11-Jun-1993
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 07/81078
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/677211
APPLICATION NUMBER: 07/677211
APPLICATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
TELEROMOUNICATION INPERMATION: NAME: LOVE, RACHART BLECOMMUNICATION INPERMATION: TELEPHONE: 41,625-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,265
FILING DATE: 2-AUG-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 22-AUG-1996
CLASSIFICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-701-265-6; Sequence 6, Application US/08701265; Patent No. 5776457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELERA: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
       South San Francisco : California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 372 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 LHKVNFY 134
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APPLICANT: Chuntha
                                                    USA
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Gaps
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%; Score 35; DB 1; Length 372; 85.7%; Pred. No. 94; tive 1; Mismatches 0; Indels
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: 11.5un-1993
FILING DATE: 11.5un-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19.DEC-1991
PRIOR APPLICATION NUMBER: 07/677211
PRIOR APPLICATION NUMBER: 07/677211
ATTORNEY AGENT INFORMATION:
NAME: LOVE, RICHARD B
REFERENCATION NUMBER: 34,659
REFERENCATION NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILLING DATE:
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-530
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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                                                                                                                                         Query Match 67.3%; Score 35; DB 2; Length 372; Best Local Similarity 85.7%; Pred. No. 94; Matches 6; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08805478

Patent No. 5874543

GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
NUMBER OF SEQUENCES:
CORRESPONDENCES:
CORRESPONDENCES:
STREET: 460 Point San Bruno Blvd
STREET: 460 Point San Bruno Blvd
STREET: California
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/76093
FILING DATE: 11-JUN-1993
FILING DATE: 11-JUN-1993
FILING DATE: 19-DEC-1991
ATTORNEY AGENT THORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REFERRENCE/DOCKET UNMBER: P0706P2PICI
TELEDPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415/952-9881
TELEX: 910/311-7168
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i LENGTH: 372 amino acids
i TYPR: Amino Acid
i TOPOLOGY: Linear
US-08-805-478-6
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-284-586-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 LHKVNFY 134
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US-08-805-478-6
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Search completed: December 16, 2003, 14:20:39 Job time : 12.3333 secs
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Sequence 5, Appli
Sequence 6647, Ap
Sequence 11, Appl
Sequence 9, Appli
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Sequence 12, Appl
Sequence 5, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 11311, A
Sequence 11311, A
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Sequence 973, App
Sequence 3, Appli
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                                                                                                                                                                 (without alignments)
75.512 Million cell updates/sec
                                                                                                                                           December 16, 2003, 14:18:11 ; Search time 22.1667 Seconds
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1: /cgn2_6/ptodate/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgr2_6/ptodate/2/pubpaa/PCT_RMW_PUB.pep:*
3: /cgr2_6/ptodate/2/pubpaa/RCT_RMW_PUB.pep:*
4: /cgn2_6/ptodate/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodate/2/pubpaa/USO6_NEW_PUB.pep:*
6: /cgn2_6/ptodate/2/pubpaa/USO8_NEW_PUB.pep:*
7: /cgn2_6/ptodate/2/pubpaa/USO8_NEW_PUB.pep:*
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9: /cgn2_6/ptodate/2/pubpaa/USO8_NEW_PUB.pep:*
10: /cgn2_6/ptodate/2/pubpaa/USO8_PUBCOMB.pep:*
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16: /cgn2_6/ptodate/2/pubpaa/USOB_PUBCOMB.pep:*
16: /cgn2_6/ptodate/2/pubpaa/USOB_PUBCOMB.pep:*
17: /cgn2_6/ptodate/2/pubpaa/USOB_PUBCOMB.pep:*
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18: /cgn2_6/ptodate/2/pubpaa/USOB_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-738-626-6647

US-09-770-089B-11

US-09-870-089B-9

US-10-015-115-107

US-09-925-300-973

US-09-995-419A-11

US-09-995-419A-11

US-09-995-419A-13

US-09-995-419A-13

US-09-995-419A-13

US-09-995-419A-13

US-09-815-242-11490

US-09-815-242-11490

US-09-815-242-11490
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                                                                                                                                                                                                                                                                                                                                                                                                   684280 segs, 185983659 residues
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Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                       Title:
Perfect score:
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                             Run on:
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67.3 372 10 US-09-104-063-6 Sequence 67.3 372 12 US-021-385-66 Sequence 67.3 372 12 US-0-221-385-66 Sequence 65.4 372 15 US-10-221-385-06 Sequence 65.4 173 372 15 US-10-221-385-06 Sequence 65.4 173 11 US-09-764-381-4446 Sequence 65.4 173 11 US-09-764-381-2446 Sequence 65.4 173 11 US-09-766-36-1 Sequence 65.4 173 11 US-09-766-36-1 Sequence 65.4 173 11 US-09-56-56-1 Sequence 63.5 10.8 19 US-09-955-373-19 Sequence 63.5 10.8 19 US-09-955-373-19 Sequence 63.5 10.8 19 US-09-951-924-0 Sequence 63.5 10.8 11 US-09-794-539-1 Sequence 63.5 10.8 10.8 10.8 10.9 10.9 10.9 10.9 10.9 10.9 10.9 10.9	Publicatión No. US20030175252A1  STRERAL/ANCORMATION:  APPLIGANTON:  APPLIGANT:  APPLICATION NUMBER:  CORRENT FILLING DATE:  AND AND APPLICATION NUMBER:  CORRENT FILLING DATE:  AND APPLICATION NUMBER:  CORRENT FILLING DATE:  AND APPLICATION NUMBER:  CORRENT APPLICATION NUMBER:  CORRENT APPLICATION NUMBER:  AND APPLICATION NUMBER:  CORRENT APPLICATION APPLICATION  A
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APPLICANT: NAKAGAWA, SATOSHI APPLICANT: NIZOGOGHI, HIROSHI APPLICANT: ANDO, SEIKO APPLICANT: HAYASHI, MIKIRO

Sequence 298, App

us-09-870-089b-5.rapb

Page 2

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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        622 FIHKVHF 628
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SOFIWAL...
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APPLICANT:
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APPLICANT:
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                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/09870089B
Publication No. US20030175252A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Charles A. Nicolette
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER FILE REFERENCE: 68126881209900
CURRENT APPLICATION UNBER: US/09/870,089B
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOGTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Charles A. Nicolette
TITLE O! INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REPREBNCE: 68126881209900
CURRENT APPLICATION UNMBER: US/09/870,089B
CURRENT FILING DATOR UNMBER: US/09/870,089B
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

Rest Local Similarity 77.8%; Pred. No. 6.1e+05;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09870089B Publication No. US20030175252A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: ATF4/CREB-2
US-09-870-089B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
               YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.5.
Pest Local 5; Conservative
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 FLHSAHFYV 30
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US-09-870-089B-11
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LENGTH: 1043
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US-09-870-089B-9
APPLICANT:
                                                                              APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-211
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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85.7%; Pred. No. 1.2e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                            Query Match 76.9%; Score 40; DB 12; Length 9; Best Local Similarity 77.8%; Pred. No. 6.1e+05; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/015,115
CURRENT FILING DATE: 2002-09-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-17
PRIOR PELING DATE: 2000-11-17
PRIOR PELING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-6
PRIOR PELING DATE: 2001-02-6
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-07-10
PRIOR PLING DATE: 2001-07-31
PRIOR PLING DATE: 2001-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 107, Application US/10015115; Publication No. US20030207800A1
GENERAL INFORMATION:
APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Drosophila melanogaster US-10-015-115-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gangolli, Esha A
Shimkets, Richard A
                                                                                                         ) OTHER INFORMATION: ATF4/CREB-2
US-09-870-089B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taupier, Raymond J
TYPE: PRT ORGANISM: Artificial Sequence
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Kekuda, Ramesha
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Best Local Similarity 85.74
Matches 6; Conservative
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APPLICANT: Geron Corporation
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
FILE REPERENCE: 083,002
CURRENT APPLICATION NUMBER: US/09/994,427A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 60/253,395
PRIOR APPLICATION NUMBER: 60/253,395
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN DATE: 2000-11-27
                           Sequence 973, Application US/09925300
; Sequence 973, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INPORMATION:
    APPLICANT: Craig Rosen,
    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
    CURRENT FILING DATE: 2001-08-10
; PRIOR PILING DATE: 2001-08-10
; PRIOR PILING DATE: 2001-08-10
; PRIOR PLING DATE: 1999-03-12
; NUMBER: OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 973
...ENGTH: 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
73.1%; Score 38; DB 10; Length 102;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 1; Indels
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US-09-995-419A-11
US-09-995-419A-11
Sequence 11, Application US/09995419A
Publication No. US20030032187A1
GENERAL INFORMATION:
APPLICANT: Genon Corporation
APPLICANT: Gold, Joseph D.
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: 096,004 - SeqList
FILE REFERENCE: 096,004 - SeqList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3, Application US/09994427A; Patent No. US20020128221A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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144 HRVHYYV 150
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RESULT 6
US-09-925-300-973
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US-09-994-427A-3
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LENGTH: 353
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APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Denning, Chris
APPLICANT: Denning, Chris
APPLICANT: Denning, Chris
APPLICANT: Clark, A. John
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
TITLE OF INVENTION: Recombination
TITLE OF INVENTION: Recombination
FILE REFERENCE: 731/002
CURRENT APPLICATION NUMBER: US/10/105,963
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/277,811
PRIOR APPLICATION NUMBER: US 60/277,811
MIMPRE OF SEA 17 NACC. A.
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APPLICANT: Geron Corporation
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
FILE REFERENCE: 083,002
CURRENT APPLICATION NUMBER: US/09/994,427A
CURRENT PILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 60/253,395
PRIOR APPLICATION NUMBER: 60/253,395
NUMBER OF SEQ. 1D NOS: 17
SOFTWARE: Patentin version 3.1
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CURRENT APPLICATION NUMBER: US/09/995,419A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 60/253,357
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 353
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SOFTWARE: Patentin version 3.1
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Matches 5; Conservative
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LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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144 HRVHYYV 150
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LENGTH: 354
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APPLICANT: Oblean, Kari L.
APPLICANT: Conserved and the conserved applicant: Tradick, John D.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROMARYOLES
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROMARY 12 2001-03-21
PRIOR PERERRAY ELITTA. 011.A
CURRENT APPLICATION NUMBER: 60/201, 078
PRIOR FILING DATE: 2000-03-21
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2001-02-16
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11311
LENGTH: 371
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                                                                                                                                                                                                                                                        Sequence 11311, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Helicobacter pylori
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Trawick, John D.
Carr, Grant J.
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Best Local Similarity 62.55
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                                                                                 145 HRVHYYV 151
3 HKVHFYV 9
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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i Sequence 14, Application US/10105963

Sequence 14, Application US/10105963

Sequence 14, Application US/10105963

Sequence 14, Application US/2030068818A1

GENERAL INFORMATION:

APPLICANT: Genoming, Chris
APPLICANT: Denning, Chris
APPLICANT: Clark, A. John

APPLICANT: Clark, J. Michael

TITLE OF INVENTION: Anianglantation and a Carbohydrate Antigens Compatible for Human

TITLE OF INVENTION: Recombination

TITLE OF INVENTION: Recombination

FILE REPERENCE: 731/002

CURRENT APPLICATION NUMBER: US/10/105,963

CURRENT FILING DATE: 2002-03-21

PRIOR FILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Version 3.1
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                                                                                                                  Query Match 69.2%; Score 36; DB 10; Length 354; Best Local Similarity 71.4%; Pred. No. 1.6e+02; Matches 5; Conservative 2; Mismatches 0; Indels
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US-09-995-419A-13
Sequence 13, Application US/09995419A
Sequence 13, Application No. US20030032187A1
GENERAL INFORMATION:
APPLICANT: GENER CONCERTION
APPLICANT: Gold, Joseph D.
APPLICANT: Gold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 14
LENGTH: 354
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
            ORGANISM: Homo sapiens
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                            ; UKGANISM: FOW
US-09-994-427A-5
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US-09-895-913A-298

Sequence 298, Application US/09895913A
Sequence 298, Application US/09895913A
Sequence 298, Application US/09895913A
Sequence 208, Application US/0960456A1
Sequence 208, Application Sequence
APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Modern Francois
APPLICANT: Modern Francois
APPLICANT: Owner, Raymond P.
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REFERENCE: 66122/043002
CURRENT APPLICATION NUMBER: US/09/895, 913A
CURRENT APPLICATION NUMBER: US/09/895, 913A
CURRENT APPLICATION NUMBER: US/09/895, 913A
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 298
LENGTH: 371
TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 67.3%; Score 35; DB 9; Length 371; Best Local Similarity 62.5%; Pred. No. 2.48+02; Matches 5; Conservative 2; Mismatches 1; Indels
Search completed: December 16, 2003, 14:41:05 Job time: 22.1667 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 LHNLHFYL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 LHNLHFYL 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LHKVHFYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-815-242-11490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-895-913A-298
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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 16, 2003, 14:10:15; Search time 10.3333 Seconds (without alignments) 83.760 Million cell updates/sec Run on:

US-09-870-089B-5 1 FLHKVHFYV 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_76:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
!: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

		₩.			SUMMARIES	
Result No.	Score	Query	Length	DB	qı	Description
-	37	71.2	099	10	279	hypothetical prote
N	36	69.2		01	S50955	
m	36	69.2		7	PC1120	٠.
4	36	69.2	353	7	A34933	glycoprotein-fucos
ß	36	69.2		N	T46126	hypothetical prote
9	36	69.2		ď	T46104	
7	36	69.2		N	860622	cytochrome-c oxida
œ	35	67.3		7	AH0655	probable regulator
σ	35	67.3		N	T32200	hypothetical prote
10	35	67.3		N	S56162	MDCR15 protein - h
11	35	67.3		7	C71952	queuine tRNA-ribos
12	35	67.3		N	A64555	tRNA-guanine trans
13	35	67.3		0	S26667	G protein-coupled
14	35	67.3		N	F64419	
15	35	67.3	569	ď	T03390	4-coumarate-CoA li
16	35	67.3		~	A82428	sensory box/GGDEF
17	35	67.3		ď	T00094	endostyle-specific
18	34	65.4		~	S41450	self-incompatibili
19	34	65.4		ď	A90546	hypothetical prote
20	34	65.4		N	B95183	
21	34	65.4		N	E98050	hypothetical prote
22	34	65.4		N	T22697	
23	34	65.4		N	T31866	hypothetical prote
24	34	65.4	m	ч	JC5644	О
25	34		m	~	842628	G protein-coupled
56	34	65.4	m	N	S32785	G protein-coupled
27	34		134	N	G71613	
28	34	65.4	1353	~≀	T19691	
29	34	65.4	1375	α	T37672	probable DNA repai

metal-regulated pr	proteinase 1, mito	hypothetical prote	probable phosphate	amino-acid ABC tra	hypothetical prote		probable c-4 methy	probable Lambda CI	B. subtilis YkrP p	B. subtilis YkrP p	hypothetical prote	conserved hypothet	hypothetical prote	diaminopimelate de	oligoendopeptidase
099695	S16817	T27466	B72757	H81391	T05665	T15451	T38986	A71365	AC1199	AI1556	F84773	AH3202	T23899	139877	G83758
~	7	7	~	~	~	7	7	7	~	2	2	~	7	7	5
153	19(	225	243	253	261	265	300	331	343	345	34.	368	430	43.	585
3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	8	3.5	3.5	3.5	63.5	3.5	63.5
Ö	ف	9	Ġ	Ġ	io	ف	Ġ	Ġ	ف	Ġ	Ġ	ю	Ġ	9	6
33	33	33	33	60	33	33	33	33	33	33	33	33	33	33	33
30	31	32	33	34	35	36	3.7	38	36	40	41	42	43	44	45

## ALIGNMENTS

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A;Map position: 1
A;Introns: 34/2; 54/2; 197/3; 283/3; 323/3; 384/1; 404/3; 452/2; 493/2; 538/2; 591/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.Kershaw, J.
submitted to the EMBL Data Library, November 1996
A.Reference number: 219617
A.Accession: T22794
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Rolecule typ
                                                                                                                                                               hypothetical protein F56H6.1 - Caenorhabditis elegans
C,Species Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C,Accession: T22794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 71.2%; Score 37; DB 2; Length 660; Local Similarity 62.5%; Pred. No. 41; less 5; Conservative 3; Mismatches 0; Indels
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RESULT 1
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620 FLHKIXFF 627 1 FLHKVHFY & ö g

Best Loca Matches

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0; Gaps

hypothetical forotein YLL065w - yeast (Saccharomyces cerevisiae) RESULT 2

NiAlternate and an analysis and protein 10536
C;Species: Saccharowyces cerevisiae
C;Species: Saccharowyces cerevisiae
C;Date: 10-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 20-Jun-2000
C;Accession: 850955; 864817
R;Wedler; H; Wambutt, R.
R;Wedler; H; Wambutt, R.
R;Wedler; H; Wambutt, R.
A;Description: Sequence of a 37 kb DNA fragment from chromosome XII of Saccharomyces cer
A;Reference number: 850950
A;Accession: 850955

A Molecule type: DNA A Residues: 1-116 (MED) A CLOSS-references: EMBL: Z47973; NID:g642313; PIDN:CAA87992.1; PID:g642319 R;Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R. submitted to the Protein Sequence Database, May 1996

A; Reference number: S64792 A; Accession: S64817

A;Molecule type: DNA A;Residues: 1-116 <WEW> A;Cross-references: EMBL:Z73170; NID:g1360279; PIDN:CAA97519.1; PID:g1360280; MIPS:YLL06 A;Experimental source: strain S288C

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C;Complex: hormodimer
C;Complex: hormodimer
C;Complex: hormodimer
C;Punction:
C;Punction:
C;Punction:
C;Punction:
C;Superfamily: histo-blood group 1 transferase
C;Superfamily: histo-blood group 1 transferase; Golgi apparatus; hexosyltransferase; polyr
C;Superfamily: histo-blood group 1 transferase; Golgi apparatus; hexosyltransferase; polyr
F;1-11/Domain: intracellular #status predicted <IVM>
F;1-37/Domain: transmembrane #status predicted <IVM>
F;12-37/Domain: trans-Golgi network lumenal #status predicted <IVM>
F;12/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Accession: T46104

R; Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, K.: submitted to the Protein Sequence Database, January 2000
A; Reference number: Z23021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein T2J13.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46126
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Mayer, Ksubmitted to the Protein Sequence Database, November 1999
                                                                                                                                                                                                                                                                                                                         A;Residues: 145-154, P',156-133 <KOM>
C;Comment: This enzyme forms group A blood type determinants from H antigen determinants
minor subtypes, for example A2 (see PIR:PC1120). Inactive alleles are responsible for gr
A; Molecule type: protein

A; Molecule type: protein

R; Residues 'X', 65-73, 'IS', 76-77 < NAV>

R; Residues 'X', 65-73, 'IS', 76-77 < NAV>

R; Kominato, Y.; McNeill, P.D.; Yamamoto, M.; Russell, M.; Hakomori, S.; Yamamoto, Y.; McOhem. Biophys. Res. Commun. 189, 154-164, 1992

Biochem. Biophys. Res. Commun. 189, 154-164, 1992

A; Title: Animal histo-blood group ABO genes.

A; Reference number: PC1164; MUID: 93080551; PMID: 1449469

A; Accession: PC1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T25B15.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Peb-2000 #sequence_revision 04-Feb-2000 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.2%; Score 36; DB 2; Length 363;
85.7%; Pred. No. 34;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: cultivar Columbia; BAC clone T2J13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:118956; OMIM:110300
A;Map position: 9q34.1-9q34.2
C;Complex: homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AL132967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 HRVHYYV 150
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Best Local Similarity
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A;Introns: 5/2; 290/3
A;Note: T2J13.120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein-fucosylgalactoside alpha-N-acetylgalactosaminyltransferase (EC 2.4.1.40) A2 N.Alternate names: histo-blood group A2 transferase (S.Species: Homo sapiens (man) (S.Species: Homo sapiens (man) (S.Species: Homo sapiens (man) (S.Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Jun-2002 (S.Accession: PC1120 (S.Yamamoto, F.; McNeill, P.D.; Hakomori, S. Biochem: Biophys. Res. Commun. 187, 366-374, 1992 (A.Fitle: Human histo-blood group A2 transferase coded by A2 allele, one of the A subtype the carboxyl terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: mRNA
A, Residues: 1-353 < YAM2>
R) Avavaratanna, N. F. Findlay, J.B.C.; Keen, J.N.; Watkins, W.M.
Bjochem. J. 271, 93-98, 1990
A; Title: Purification, properties and partial amino acid sequence of the blood-group-A-9
A; Reference number: S13173; MUID:91024951; PMID:2121135
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A.Reference number: 809593; MUID:90238543; PMID:2333095
A.Accession: 809593
A.Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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                                                                                                                                                                                                                                                                                              Gaps
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A;Redidues: 1-255 <4NA
A;Redidues: 1-255 <4NA
A;Cross-references: GB:844054; NID:9255066; PIDN:AAB23167.1; PID:9255067
C;Superfamily: histo-blood group 1 transferase
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-353 <YAM1>
A;Residues: 1-353 <YAM1>
A;Cross-references: GB:J05175; NID:g340077; PIDN:AAA36792.1; PID:g340078
R;Yamamoto, F.I.; Clausen, H.; White, T.; Marken, J.; Hakomori, S.I.
Nature 345, 229-233, 1990
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                                                                                                                                                                                                         69.2%; Score 36; DB 2; Length 116; 75.0%; Pred. No. 11; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.2%; Score 36; DB 2; Length 295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: PC1120; MUID:92392351; PMID:1520322 A;Accession: PC1120
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.4%; Pred. No. 28;
tive 2; Mismatches
        C;Genetics:
A;Gene: SGD:GIN11
A;Coss-references: SGD:S0003988; MIPS:YLL065w
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                                                                                                                                                                                                                                                      Local Similarity 75.0 hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 FTHKVHHY 53
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A;Status: preliminary
                                                                                                                                      A; Map position: 12L
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cibate: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
Cibate: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
Cibates and Cibates an
th, T.; Connerton, P.; Cronin, A.; Davie, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 846-852, 2001
Ajauthora: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., Ajauthora: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., Ajatte: Complete genome sequence of a multiple drug resistant Salmonella enterica seron Ajacesesion: AH0655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AP022979; PIDN:AAB69902.1; GSPDB:GN00023; CESP:T02B11.4
A;Experimental source: strain Bristol N2; clone T02B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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A;Molecule type: DNA
A;Residues: 1-250 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08427.1; PID:g16502470; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32200
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C;Superfamily: vertebrate rhodopsin
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Local Similarity 62.5%; Pred. No. 36;
Local Sciniarity 62.5%; Pred. No. 36;
Local Sciniarity 62.5%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 67.3%; Score 35; DB 2; Length 250; Local Similarity 71.4%; Pred. No. 36; Conservative 2; Mismatches 0; Indels
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47;
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Ajbesoription: The sequence of C. elegans cosmid T02Bll.
A;Reference number: 221135
A;Accession: T32200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T02B11.4 - Caenorhabditis elegans
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85.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: regulatory protein gutR
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A;Introns: 47/3; 69/1; 92/1; 180/2
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Best Local Similarity
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A,Gene: STY1347
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A;Accession: S60624
A;Acseducas: L-512 < VAL.
A;Cross-references: EMBL;X69067; NID:g505262; PIDN:CAA48806.1; PID:g578437
B;Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.
A;Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and par A;Reference number: S60624; MUID:94223692; PMID:8169960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AH0655
probable regulatory protein STY1347 [imported] - Salmonella enterica subsp. enterica ser C.Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology C;Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-ae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
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F;9455/Domain: cytochrome-c oxidase chain I homology <COl>
F;9455/Domain: cytochrome-c oxidase chain I homology <COl>
F;59,376/Binding site: here a iron (His) #status predicted
F;238,288,289/Binding site: copper (His) #status predicted
F;238-242/Cross-link: 1'-histidyl-7'-tyrosine (His-Tyr) #status predicted
F;245/Binding site: oxygen (Tyr) #status predicted
F;366/Binding site: magnesium (His) (#shared with chain II) #status predicted
F;347/Binding site: heme a3 iron (His) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytochrome-c oxidase (BC 1.9.3.1) chain I - brine shrimp mitochondrion C; Species: mitochondrion Artemia franciscana (brine shrimp)
C; Date: 23-Feb-1996 #sequence_revision 26-Jul-1996 #text_change 07-Dec-1999
C; Accession: 560622; S60638
R; Valverde, J.R.
Submitted to the EMBL Data Library, June 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                               A;Introns: 20/3; 155/3; 220/3; 317/1; 369/1; 384/3
A;Note: T25B15.110
C;Superfamily: Arabidopsis thaliana hypothetical protein F24B22.230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
69.2%; Score 36; DB 2; Length 412;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                       A)Experimental source: cultivar Columbia, BAC clone T25B15 C,Genetics:
A,Map position: 3
                                                                   A,Molecule type: DNA
A,Residues: 1-412 <ALC>
A,Cross-references: EMBL:AL132972
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A;Residues: 146-311 <PER>
A;Cross-references: EMBL:X69067
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Matches 6; Conservative
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A; Genetic code: SGC4
              A; Status: preliminary
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us-09-870-089b-5.rpr

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hypothetical protein MJ0958 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Jacession: F64419
R;Bult, C;J.; White, O.; Olsen, G;J.; Zhou, L;Fleischmann, R.D.; Sutton, G;G.; Blake, R;Bult, C;J.; Write, O.; Orstbeek, R;Krhess, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; redoh, C;L; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:9633799; PMID:8688087
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Cidatesion: T0390
Rizhao, Y.; Kung, S.D.; Bottino, P.J.
submitted to the EMBL Data Library, July 1995
A) Bosoription: 4-Coumarate: CoA ligase genes in rice: divergent structure and differenti
A; Reference number: 214921
A; Accession: T03390
R.Dobner, T.; Wolf, I.; Emrich, T.; Lipp, M.

Eur. J. Immunol. 22, 2795-2799, 1992

A,Title: Differentiation-specific expression of a novel G protein-coupled receptor from A;Reference number: $26667; WUID:93049615; PMID:1425907

A,Accession: $26667
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A;Residues: 1-569 <ZHA>
A;Cross-references: EMBL:L43362; NID:g893293; PIDN:AAA69580.1; PID:g893294
C;Genetics:
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A;Modecule type: DNA
A;Residues: 1.372 - GODB>
A;Cross-references: EMBL:X68149; NID:g29459; PIDN:CAA48252.1; PID:g29460
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C;Superfamily: Methanococcus jannaschii hypothetical protein MJ0958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.3%; Score 35; DB 2; Length 372; Best Local Similarity 85.7%; Pred. No. 54; Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross.references: GDB:136235; OMIM:601613
A,Map postition: 15q26.1-15q26.1
C,Superfamily: vertebrate rhodopsin
C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor; transmembrane protein
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128 LHKVNFY 134
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Ariele: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                            queuine tRNA-ribosyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Avariety: strain J99
C;Accession: C71952
C;A
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A;Reference number: A71800; MUID:99120557; PMID:9923682
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A,Residues: 1-371 <ARN>
A,Cross-references: GB-AE001464; GB:AE001439; NID:g4154789; PIDN:AAD05847.1; PID:g415479
A;Experimental source: strain J99
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A,Residues: 1-371 <TOO.
A;Crosa-references: GB.AE000547; GB:AE000511; NID:g2313377; PIDN:AAD07350.1; PID:g231337
C;Superfamily: queuine tRNA-ribosyltransferase
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G protein-coupled receptor BLR1 - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: $26667
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 29-Sep-1999
C;Accession: A64555
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LRNA-guanine transglycosylase - Helicobacter pylori (strain 26695)
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                   0; Indels
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A.Gene: tgt
C.Superfamily: queuine tRNA-ribosyltransferase
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Matches 5; Conservative
              6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LHKVHFYV 9
                                                                                                                                                                                              83 LHKVNFY 89
                                                                                                             2 LHKVHFY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: C71952
A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                       Matches
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A;Note: 4cl.2 C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology C;Keywords: acid-thiol ligase; coensyme A; flavonoid biosynthesis F;89-562/Domain: acetate-CoA ligase homology <ACL>

0; Gaps Query Match
67.3%; Score 35; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels

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2 LHKVHF 7 |||||| 540 LHKVHF 545 ò

Db

Search completed: December 16, 2003, 14:19:14 Job time : 11.3333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 16, 2003, 14:06:35; Search time 5.6667 Seconds (without alignments)
74.689 Million cell updates/sec Run on:

US-09-870-089B-5 1 FLHKVHFYV 9 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	ind seinofed Annyoo	bacterion					P16442 h histo-blo					008314 helicobacte							Q04683 mus musculu	P34997 rattus norv	Q9ghg9 acorus cala	P37960 bacillus su	P28627 saccharomyc		4	N	m	4,	098635 nuphar vari		Q8wjr9 arpophyllum		Q9ghe5 zantedeschi
ID	MATE HELBIT	YOSI BPT4	MATK_TRILU	MATK_TRIUN	MATK TRIMC	L100_ADECC	BGAT_HUMAN	MATK_KUNCA		COX1_ARTSF	TGT HELPJ	TGT_HELPY	CCRS_HUMAN	Y958 METJA	MATK_ARUDI	4CL2_ORYSA	PTE1_HUMAN	TRMU_BUCBP	CCRS_MOUSE	CCRS_RAT	MATK_ACCAL	MRGA_BACSU	IMP1_YEAST	GIDB_STRMU	ER25_SCHPO	HFLC_TREPA	DCDA_BACMT	MATK BRASC	MATK NUPVA		MATK_ARPGI		MATK_ZANAE
DB	-	-	Н				П	Н	~	Н	-	۲	Н	Н					Н										-	Н	Н	Н	1
Length	7.77	181	515	515	517	689	354	202	505	512	371	371	372	426	504	269	319	370	374	374	511	153	189	237	300	331	432	200	505	507	509	509	512
% Query Match	9 30							69.2									65.4	65.4		65.4	65.4	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5		
Score	1 0 5	3.7	37	37	37	37	36	36	36	36	35	35	35	35	35	35	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33
Result No.	1	10	m	4	S	9	7	80	6	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

181 AA.

PRT;

STANDARD;

Y05I\_BPT4 ID Y05I\_BPT4 S AC P39240; Q96215;

RESULT 2

Q9ghb2 phoenix dac Q9tna5 aspidistra	Q9tnbl convallaria Q99mv7 mus musculu	Q07868 bacillus su Q9pke6 chlamydia m	OB4250 chlamydia t O18115 caenorhabdi	Q89a41 buchnera ap P94525 bacillus su	P39907 bacteroides	•
MATK_PHODC MATK_ASPEL	MATK_CONMJ RN17_MOUSE	PBPB_BACSU PHSG_CHLMU	PHSG_CHLTR	RS6 BUCBP ARAD BACSU	LPSA_BACNO	
<b>~</b>			н н		Н г	4
514	520 626	716 813	814	119	318	i :
63.5	63.5 63.5	63.5	63.5	61.5	61.5	
333	333	333	333	2 2 2	32	3
3.4 5.5	36 37	8 6 6 7	4041	4 4	4 4 4 A	?

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                                                                                                                                                                                               Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;
                                                                                                                                                                                                                                                                                                                          Kazempour Osaloo S., Utech F.H., Ohara M., Kawano S.,
"Molecular systematics of Trilliaceae I. Phylogenetic analyses of
Trillium using marK gene sequences.";
J. Plant Res. 112.35-49(1999.";
-1- FUNCTION: Probably assists in splicing chloroplast group II
introns (By similarity).
-1- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.9%; Score 40; DB 1; Length 515; 66.7%; Pred. No. 4.1; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK N; 1.
mRNA_processing; Chloroplast.
SEQUENCE 515 AA; 61546 WW; D6C14A5AB0DA468F CRC64;
                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB017375; BAA36791.1; -.
AnterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MatK_N.
                                                                                                                                                            Helonias bullata (Swamp pink).
                                                                                                                          Maturase K (Intron maturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 66.73
Matches 6, Conservative
                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || ::||||
247 FLERIHFYV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FLHKVHFYV 9
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         NCBI_TaxID=50364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY.
                                                                                                                                                                                Chloroplast.
                                                                                                                                                                                                                                                                                                                  TISSUE=Leaf
                                 MATK HELBU
                                                                                                                                                                                                                                       Helonias.
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                                                   O9XPN6;
             MATK_HELBU
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                             Maharia N., Marusich E., Djavakhishvili T., Neitzel J., Peterson S., Awaya M., Eidermiller J., Canada D., Tracy J., Gailbreath K., Paddison P., Anderson B., Stidham T., Blattner F., Kutter E.M., "The 10.7 kb' nonessential' region of bacteriophage T4 between the genes tk and nrdC: twenty new t4 genes, generally conserved among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Trilliaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kazengur Osaloo S., Utech F.H., Ohara M., Kawano S.,
"Molecular systematics of Trilliaceae I. Phylogenetic analyses of
Trilliam using matK gene sequences.";
J. Plant Res. 112:35-49(1999).
-!- FUNCTION: Probably assists in splicing chloroplast group II
introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
-!- SIMILARITY:
                                                                            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
01-FEB-1995 (Rel. 31, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
48-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 211 kDa protein in mobD-ri intergenic region.
YOSI OR MOBD.1 OR TK.-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.2%; Score 37; DB 1; Length 181; 83.3%; Pred. No. 5.1; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                   Kutter E., Arieaka F., Kunisawa T., Tsugita A., Mosig G., Mesyanzhinov V., Ruger W., Stidham T., Thomas E.; Bacteriophage T. genome analysis ", Submitted (JUL-2000) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                   T-even phages,";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 181 AA; 21177 WW; E51430751E2EAF3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [5-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trillium luteum (Yellow wakerobin).
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U76612; AAB26969.1; -.
EMBL; AF158101; AAD42593.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maturase K (Intron maturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 83.3
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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65 HKIHFY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=82489;
                                                                                                         NCBI_TaxID=10665;
                                                                 Bacteriophage T4.
                                                                                            r4-like viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rissue=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-SEP-2003
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                   between the Swism Institute of Bioinformatics and the EMBL outstation—
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or send an email to license@isb-sib.ch).
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Trilliaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kazempour Osaloo S., Utech F.H., Ohara M., Kawano S.; Molecular systematics of Trilliaceae I. Phylogenetic analyses of Trillium using matK gene sequences."; J. Plant Res. 112:35-49(1999).

-!-FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).

-!-SUMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.2%; Score 37; DB 1; Length 515; 66.7%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1; Length 515;
Pred. No. 15;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF01348; Intron maturas2; 1.
Pfam, PF01824; MatK N; 1.
mRNA processing; Chloroplast.
SEQUENCE 515 AA; 61306 MW; 1CB6F63DFB45AED4 CRC64;
                                                                                                                                                                                                                                                                                                                                           Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK N; 1.
mRNA, processing; Chloroplast.
SEQUENCE 515 AA; 61074 MW; 6D750AF7P444DB50 CRC64;
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MATK TIUN STANDALL,
MATK TIUN STANDALL,
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rrillium undulatum (Painted trillium).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AB017413; BAA36829.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK N.
                                                                                                                                                                                                                                              EMBL; AB017396; BAA16812.1; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MatK. N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.28;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.73
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 FLERTHFYV 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=82504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Trilliaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kazempour Osaloo S., Utech F.H., Ohara M., Kawano S.; "Molecular systematics of Trilliaceae I. Phylogenetic analyses of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trillium using matK gene sequences.";
J. Plant Res. 112:35-49(1999).
-!- FUNCTION: Probably assists in splicing chloroplast group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       introns (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.2%; Score 37; DB 1; Length 517; 66.7%; Pred. No. 15; 2; Indels iive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK N; 1.
mRNA processing; Chlorolast.
SEQUENCE 517 AA; 61378 MW; C18AB9643A7B5FED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Maturase K (Intron maturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Late 100 kDa protein.
Canine adenovirus type 1 (strain CLL), a
Canine adenovirus type 1 (strain RI261)
                                                                                                                                                                                                                                                                                                                 Trillium maculatum (Spotted wakerobin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB017397; BAA36813.1; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MatK.N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campbell J.B., Zhao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 FLERTHFYV 255
                                         247 FLERTHFYV 255
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1 FLHKVHFYV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=82490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Leaf
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J. Biol. Chem. 265:1146-1151(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein-fucosylgalactoside alpha-N-acetylgalactosaminyltransferase (EC 2.4.1.40) (Fucosylglycoprotein alpha-N-acetylgalactosaminyltransferase) (Histo-blood group A transferase) (A transferase); Glycoprotein-fucosylgalactoside alpha-galactosyltransferase (EC 2.4.1.37) (Fucosylglycoprotein 3-alpha-galactosyltransferase) (Histo-blood group B transferase) (B
                                                                                                                                                                  Morrison M.D., Onions D.E., Nicolson L., "Complete DNA sequence of canine adenovirus type 1."; J. Gen. Virol. 78:873-878 (1997).
--i- FUNCTION: THE 100 kDa PROTEIN IS A LATE NONSTRUCTURAL PROTEIN INVOLVED IN TRANSPORT OF HEXON FROM CYTOPLASM TO THE NUCLEUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarthini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90238543; PubMed=2333095;
Yamamoto R.-I., Clausen H., White T., Marken J., Hakomori S.-I.;
"Molecular genetic basis of the histo-blood group ABO system.";
Nature 345:229-233(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P16442; Q14490;
01-AUG-1990 (Rel. 15, Created)
01-DEC-1992 (Rel. 24, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Histo-blood group ABO system transferase (NAGAT) [Includes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.2%; Score 37; DB 1; Length 689; 83.3%; Pred. No. 20; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=90110099; PubMed=2104828;
Yamamoto F.-I., Marken J., Tsuji T., White T., Clausen H.,
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77373 MW; 6062D58E0ACE7763 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 AA.
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MEDLINE=95118355; PubMed=7598760;
                                                                                                                                        MEDLINE=97275900; PubMed=9129661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR03381; Adeno 100.
Pfam; PF02438; adeno 100; I.
Late protein; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, US5001; AAB05446.1; -.
EMBL, Y07760; CAA69039.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 83.3 tes 5; Conservative
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                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                              GO:0005576; C:extracellular; NAS.
GO:0001017; C:integral to GOIGi membrane; NAS.
GO:0004381; F:glycoprotein-fucosylgalactoside alpha-galac. .; NAS.
GO:0004380; F:glycoprotein-fucosylgalactoside alpha-N-ace. .; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTECLYTIC PROCESSING.
POLYMORPHISM: THE SEQUENCE SHOWN IS THAT OF THE A TRANSFERASE. THE
B FORM DIFFERS BY A FEW RESIDUES SUBSTITUTIONS, THE O PHENOTYPE IS
RESULT OF A SINGLE BASE FRAMESHIFT DELETION IN THE N-TERMINAL
EXTREMITY OF THE GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IN TRANS CISTERNAE OF GOLGI. SOLUBLE FORM IN BODY FLUIDS.
                    Geurts van Kessel A.;
Machomic cloning of the human histo-blood group ABO locus.";
Micchem. Biophys. Res. Commun. 206:318-325(1995).
                                                                                       MEDLINE=95298046; PubMed=7779106;
Bennett E.P., Steffensen R., Clausen H., Weghuis D.O.,
Geutts van Kessel A.;
"Genomic cloning of the human histo-blood group ABO locus.";
Biochem. Biophys. Res. Commun. 211:347-347(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
                                                                                                                                                                                                                      "Human histo-blood group ABO gene locus alleles.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
Bennett B.P., Steffensen R., Clausen H., Weghuis D.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X84746; CAA59233.1; -. EMBL; X84747; CAA59233.1; JOINED. EMBL; X84748; CAA59233.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X84750, CAA59233.1, JOINED.
EMBL, X84751, CAA59233.1, JOINED.
EMBL, X84752, CAA59233.1, JOINED.
                                                                                                                                                                                                                                                                                  MEDLINE=91035461; PubMed=2121736;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF134412; AAD26572.1; -. EMBL; AF134413; AAD26573.1; -. EMBL; AF134414; AAD26574.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J05175; AAA36792.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 1LZ0; 28-AUG-02.
PDB; 1LZ1; 28-AUG-02.
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                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Myrtales; Myrtaceae; Kunzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'Brien M.M., Quinn C.J., Wilson P.G.; "Molecular Systematics of the Leptospermum suballiance (Myxtaceae).";
                                                                                    FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE, SOLUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                             SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                    LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aust. J. Bot. 48:621-628(2000).
-!- FUNCTION: Probably assists in splicing chloroplast group II introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                       /FTId=VAR 003410.

G -> S (IN GROUP B TRANSFERASE).
/FTId=VAR 003410.

J -> M (IN GROUP B TRANSFERASE;
IMPORTANT FOR THE SPECIFICITY).
/FTId=VAR 003412.

G -> A (IN GROUP B TRANSFERASE;
IMPORTANT FOR THE SPECIFICITY).
/FTId=VAR 003413.
              InterPro, IPR005076; Glyco trans_6.
Pfam, PP03414; Glyco transf_6.
Transferase; Glycoprotein; Transmembrane; Signal-anchor; Golgi stack; Polymorphism; Blood group antigen;
                                                                                                                                                                                                                              P -> L (IN ALLELE A2).
/FTId=VAR 003409.
R -> G (IN GROUP B TRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                            R -> W (IN ALLELE B3 OF GROUP B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 1; Length 354;
Pred. No. 15;
2; Mismatches 0; Indels
GO; GO:0006486; P:protein amino acid glycosylation; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 354 AA; 40934 MW; A03DA16E630C1608 CRC64;
                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                  FTIG=VAR 003408.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kunzea capitata (Pink kunzea).
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Similarity 71.4%;
5; Conservative 2
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113
81
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53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 HKVHFYV 9
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                                                                         3D-structure.
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TRANSMEM
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"Molecular systematics of the Leptospermum suballiance (Myrtaceae).";
Aust. J. Bot. 48:621-628(2000).
-!- FUNCTION: Probably assists in splicing chloroplast group II
introns (By similarity).
-!- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
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0
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                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                      EMBL; AF184723; AAF05930.1; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR00286; Mark N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01348; Mark N.; 1.
Rfam; PF04824; Mark N.; 1.
SEQUENCE 505 AA; 60711 MW; 41B5EC246DC096A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ssing; Chloroplast.
505 AA; 60657 MW; 20D2B47963263B8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Welrber, 2003 (Rel. 41, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
   or send an email to license@isb-sib.ch).
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InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MarK N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maturase K (Intron maturase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunzea ericoides (Kanuka).
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.0.
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 FFERIHFYV 246
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238 FFERIHFYV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FLHKVHFYV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA processing;
SEQUENCE 505 AZ
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COXI ARTSF
ID COXI ARTSF
AC Q37705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MATK KUNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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MATTRE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94223692; PubMed=8169960;

Percz M.L., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;

Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic brine shrimps.";

J. Mol. Evol. 38:156-168(1994).

-!- FUNCTION: CYTOCHOME C OXIDAGE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME COMPLEX. CO I IS THE CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEMB A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME AS AND COPPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --!- PATHWAY: Respiratory chain; terminal step.
--- SUGCELLAR LOCATION: INTEGRAL MENBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.
--- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
IRON (HEME A AXIAL LIGAND) (PROBABLE).
IRON (HEME A AXIAL LIGAND) (PROBABLE).
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                                                                                                                             Bukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
Artemiidae; Artemia.
NCBI TaxID=6661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON (HEME A AXIAL LIGAND) (PROBABLE).
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                                                                        CÓI OR CO-I.
Artemia sanfranciscana (Brine shrimp) (Artemia franciscana).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COX1; 1.
Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.2%; Score 36; DB 1; Length 512; 66.7%; Pred. No. 22; 1; Indels ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4AA1E1BBE64913E3 CRC64;
15-UUL-1998 (Rel. 36, Dreated)
15-UUL-1998 (Rel. 36, Dreat sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cytochrome c oxidase polypeptide I (EC 1.9.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGT HBLPJ STANDARD; PRT; 371 AA Q9ZNF4; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory chain; Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56491 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X69067; CAA48806.1; -. PIR; S60622; S60622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P00396; 20CC.
InterPro; IPR000883; COXI.
Pfam; PF00115; COXI; 1.
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376 3
238 2
512 AA;
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es 6; Conser
                                                                                                                                                                                                            SEQUENCE FROM N.A.
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CROSSLNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- ČOFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SIMILARITY: BELONGS TO THE QUEUINE TRNA-RIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAS with GU(N) anticodons (tRNA-Asp, -Asn, -His and -Tyr). After this exchange, a cyclopentendiol moiety is attached to the 7-aminomethyl group of 7-deazaguanine, resulting in the hypermodified uncleoside queucaine (Q) (7-(((4,5-cis-dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine) (By
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guld B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999)
                                                                                                      Helicobacter pylori 399 (Campylobacter pylori 399).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NGBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: tRNA guanine + queuine = tRNA queuine +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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RESP, P28720; C71952.
HSSP, P28720; LPUD.
RINGERPO, IPRO04803; ORRNA_ribo_trans.
InterPro; IPR004803; ORRNA_ribo_trans.
R Pfam, PP01702; TGT7; 1.
R TIGREAMS; TIGRO049; QLRNA_tgt; 1.
CQUBOSING blosynthesis; Transferase; Glycosyltransferase; MLRNA_processing; Zinc; Complete proteome.
R ACT SITE 266 266 BY SIMILARITY.
RACT_SITE 266 266 BY SIMILARITY.
28-FEB-2003 (Rel. 41, Last annotation update)
Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (tRNA-guanine
transglycosylase) (Guanine insertion enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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303 303 ZII
305 305 ZII
308 ZIII
334 334 ZIII
371 AA; 41506 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.3%;
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es 5; Conservative
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                                                                                                                                                               STRAIN=26695 / ATCC 700392;
STRAIN=26695 / ATCC 700392;
MEDLINE=37934467; PubMed=9252185;
Tomb U.-F., White D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Rleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush U., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Goodson D., Dutterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Pujii C., Bowman C., Watthey L., Wallin B., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SIMILARITY: BELONGS TO THE QUEUINE TRNA-RIBOSYLTRANSFERASE FAMILY.
                                                                                 Bacteria; Profeobacteria; Epsilonprofeobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: tRNA guanine + queuine = tRNA queuine +
28-FEB-2003 (Rel. 41, Last annotation update)
deutine tRNA-ribosyltransferase (EC 2.4.2.29) (tRNA-guanine transglycosylase) (Guanine insertion enzyme).
TGT OR HP0281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGRO0430; O_tRNA_tgt; 1.
TIGRFAMS; TIGRO0449; tgt general; 1.
Queuosine biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
N -> KH (IN STRAIN P1).
N -> D (IN STRAIN P1).
A -> V (IN STRAIN P1).
E -> G (IN STRAIN P1).
E -> G (IN STRAIN P1).
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ACT_SITE 91 91 91 SY SIMILARITY.
ACT_SITE 266 266 BY SIMILARITY.
                                                                     Helicobacter pylori (Campylobacter pylori).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000847; AAD07350.1; -...
EMBL; Y12061; CAA72784.1; -...
FIR; A64555, A64555.
HSSP; P28720; 1PUD.
TICR; HP0281; -...
HAMAP; MF 00168; -; 1.
HAMAP; MF 00168; -; 1.
HAMAP; MF 01028; -; PF0004803; OtrnA_ribo_trans.
InterPro; IPR002616; tRNA_ribo_trans.
Pfam; PF01702; TGT; 1.
                                                                                                                                                                                                                                                                                                                                                                              Nature 388:539-547(1997).
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308
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338
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118
466
788
788
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                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=210;
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                                                                                                                                                                                                                                                                                                                               Venter J.
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01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 5 (CXC-R5) (CXCR-5) (Burkitt'S lymphoma receptor 1) (Monocyte-derived receptor 15) (MDR15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: CYTOKINE RECEPTOR THAT BINDS TO BLC. BIRI EXERTS
POSSIBLY A REGULATORY FUNCTION IN BURKITT LYMPHOWA (BL)
LYMPHOWAGENESIS AND/OR B-CELL DIFFERENTIATION. IT IS A POTENTIAL
CANDIDATE FOR CELL-CELL INTERACTION, AND ACTIVATION OF MATURE B-
LYMPHOCYTES IN LYMPHATIC TISSUES.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- ALTERNATIVE PRODUCTS:
EVENT. BATTER B-
EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Lymphocytes;

BIDLINE-93049615; PubMed=1425907;

Dobner T., Wolf Intich T., Lipp M.;

Differentiation-specific expression of a novel G protein-coupled receptor from Burkit's lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barella L., Loetscher M., Tobler A., Baggiolini M., Moser B.; "Sequence variation of a novel heptahelical leucocyte receptor through alternative transcript formation."; Blochem. J. 309:773-779(1995).
                                                                                                                                                                                                                                                                                                                                DB 1; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                1; Indels
G -> V (IN STRAIN PI).
Y -> Q (IN STRAIN PI).
Y -> G (IN STRAIN PI).
D -> G (IN STRAIN PI).
K -> N (IN STRAIN PI).
K -> N (IN STRAIN PI).
K -> N (IN STRAIN PI).
E -> K (IN STRAIN PI).
B -> K (IN STRAIN PI).
A -> T (IN STRAIN PI).
B -> K (IN STRAIN PI).
A -> T (IN STRAIN PI).
B -> T (IN STRAIN PI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 AA.
                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                                                                                                                                                                                                                                                                                                67.3%; Score 35; 62.5%; Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM LONG).
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                                                                                                                                                                                                                                                                                      41415 MW;
                                                                                                                                                                                                                                                                                                                                                         Local Similarity 62.5
les 5; Conservative
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       76
84
108
1120
1177
1181
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258
304
371 AA;
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                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM, 601613; -. Gintegral to plasma membrane, TAS. GO; GO:0005887. C:integral to plasma membrane, TAS. GO:0006928; P:cell motility; TAS. GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS. InterPro; IPR000276; GPCR_Rhodpsn.
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                                                      LYMPHOMA CELLS.
-:- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G ROOTEIN RECEP_F1 1; 1.

PROSITE; PS00262; G PROTEIN RECEP_F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell;

Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
isold=P32302-2; Sequence=VSP 001892;
SGUE SPECIFICITY: EXPRESSION MATURE B-CELLS AND BURKITT
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/FTId=VSP_001892.
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Archaea, Euryarchaeota, Methanococci, Methanococales,
Methanocaldococcaceae, Methanocaldococcus.
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0958 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                   EMBL; X6829; CAA48723.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S26667; S26667.
Genew; HGNC:1060; BLR1.
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109
124
145
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TRANSMEM
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                                                                                     MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutron G.G., Blake J.A., Tilleferald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick V.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weinston J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Rosaceae incertae sedis; Aruncus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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-i- SIMILARITY: BELONGS TO THE INTRON MATURASE FAMILY 2. MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potter D., Gao F., Oh S.-H., Baggett S.; "Phylogenetic relationships among putative genes encoding polygalacturonse inhibitor proteins (PGIPs) in Rosaccae."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 35; DB 1; Length 426; 57.1%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL PROTEIN MJ0958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Signal; Complete proteome. SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                             SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aruncus dioicus (Goat's beard)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U67539; AAB98971.1; -. PIR, F64419; F64419.
TIGR; MJ0958; -.
                                                                                                                                                                                                                                                                                                                                                       Jannaschii.";
Science 273:1058-1073(1996).
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 HKLHYYI 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=32220;
NCBI_TaxID=2190;
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Q8WJR4;
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Q9cwl2 mus musculu
9vhm2 drosophila
960b2 drosophila
                             homo sapien
homo sapien
pisolithus
                                                                                                                           dendrophyla
harrisella
harrisella
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paris thibe
29bt16 homo sapien
                                                                                                    caenorhabdi
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daiswa thib
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trillium lu
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                                                                       siphonochil
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                                                               campylobact
                                                                                      plasmodium
                                                                                              plasmodium
                                                                                                                                                                                                            trillium ]
kinugasa j
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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005283; BAC00249.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 1043 AA; 112335 MW; 2A44C0E5431A29FC CRC64;
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                                                             Q8kwr1
Q8hv19
Q81389
Q81389
Q81345
Q94512
Q8kqw4
Q8hrj5
Q8hrj4
Q8hrj3
Q8hrj3
Q8hrj3
Q8hrj3
                                                                                                                                                                             09spn8
09ghc4
09xr22
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09xpp0
09xr21
                                              Q9xlp0
Q9xln5
                               Q8wx49
                                                                                                                                                                                                                                                                                                                                                 Corymebacterium glutamicum (Brevibacterium flavum).
Bageria, Actinobacteria, Actinobacteridae; Actinomycetales;
Osrymebacterineae; Corynebacteriaceae; Corynebacterium.
WCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 82.7%; Score 43; DB 16; Length 1043; Local Similarity 77.8%; Pred. No. 13; Assarches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                         01-0CT-2002 (Tremairel. 22, Created)
01-0CT-2002 (Tremairel. 22, Last sequence update)
01-0CT-2002 (Tremairel. 22, Last annotation update)
Hypothetical membrane protein Cgl2855.
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Last annotation update)
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                     ALIGNMENTS
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
                     Q960B2
Q8WX49
Q9WX49
Q9XLN5
Q8KWR1
Q8HV19
Q8HV18
Q81389
Q81389
Q81389
Q8GS12
Q9GS12
Q9GS12
Q8HRJ4
Q8HRJ4
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      Q9CWL2
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Q9XPN8
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Q9XPP3
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               Q9VHM2
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                             FLHSAHFYV 30
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Q9GHD1;
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QBNLT2
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Q9GHD1
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chionograph
heloniopsis
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heloniopsis
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Q9ghd5 heloniopsim
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                                                     December 16, 2003, 14:09:45; Search time 25 Seconds (without alignments) 92.899 Million cell updates/sec
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08hv35
09ghc6
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      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                      - protein search, using sw model
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Q9GHC9
Q9GHC8
Q9GHC8
Q9GHD3
Q9GHD6
Q9GHD6
Q9GHD6
Q9GHD7
Q9GHD7
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Q8HV35
Q9GHC6
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sp_mammal:*
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sp_organelle:*
sp_phage:*
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sp_virus:*
sp_vertebrate:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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Maximum DB seq length: 2000000000
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Match Length DB
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Tue Dec 16 15:00:22 2003

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Lefuntion: PROBABLY ASSISTS IN SPLICING CHLOROPLASTS GROUP II INTRONS (BY SIMILARITY)

C.I. SIMILARITY: WITH CORRESPONDING ORP IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY CHOCHONDRIAL INTRONS.

C. MINCHONDRIAL INTRONS.

DR. INTERPRO; IPRO02466; Matk N.

DR. InterPro; IPRO02442; Intron maturase2.

DR. InterPro; IPRO02442; Intron maturase2.

DR. Féam; PP01348; Intron maturase2.

DR. Féam; PP01348; Intron maturase2; 1.

PR Féam; PP01824; Matk N: 1.

From: PF01824; Matk N: 1.

From: FF01824; Matk N: 1.

From: FF01824; Matk N: 1.
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                                                                                                                                                                                                                                                                                                                                            STRAIN=yellow flower;
Fuse S., Tamura M.N.;
Ruge S., Tamura M.N.;
Ruge S., Tamura M.N.;
Ruge S., Tamura M.N.;
Ruge S., Tamura M.N.;
Relanthiaceae sensu lato.";
Plant Biol. 2:415-4712000).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
-!- AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
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Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
                                                                                                                                 Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.9%; Score 40; DB 8; Length 515; 66.7%; Pred. No. 24; ive 2; Mismatches 1; Indels
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InterPro; IPR000442; Intron maturse2.
InterPro; IPR00286; Mark N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; Mark N.) 1.
BRNA processing; Chloroplast.
SEQUENCE 515 AA; 61747 MW; 66A8AllDDA39BFBB CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Intron maturase (Maturase K)
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                                                                      Heloniopsis orientalis
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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGICNS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED F
MITOCHONDRIAL INTRONS.

EMBL, AB040194; BAB16802.1; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; Matk N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01348; Intron maturas2; 1.
mRNA processing; Chloroplast.
SEQUENCE 515 AA; 61886 MW; 495C06AD09F7FE66 CRC64;
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"A phylogenetic analysis of the plastid matK gene with emphasis on balanthiaceae sensu lato.";
Plant Biol. 2:415-427 (2000).
-i- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
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Fuse S., Tamura M.N.;
A phylogenetic analysis of the plastid matK gene with emphasis on Melanthiaceae sensu late. ";
Plant Biol. 2:415-427(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
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                             Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Intron maturase (Maturase K).
                                                                                                                                                                                                                                                                                                               515 AA
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Best Local Similarity 66.7%; Pred. No. 24; Matches 6; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Intron maturase (Maturase K).
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                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heloniopsis orientalis.
                                                                                                                                247 FLERIHFYV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 FLERIHFYV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heloniopsis umbellata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FLHKVHFYV 9
                                                                                            1 FLHKVHFYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=pink flower;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=87628;
                                                                                                                                                                                                                                                                                                                                            O9GHC9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09GHC8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9GHC8
                                                                                                                                                                                                                                                                                                               63HD60
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                                                                                                                                                                                                                                                RESULT 4
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Query Match
Best Local Similarity
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"A phylogenetic analysis of the plastid matk gene with emphasis on malauthiaceae ensus late.";

"A phylogenetic analysis of the plastid matk gene with emphasis on melanthiaceae ensus late.";

"B phylogenetic analysis of the plastid matk gene with emphasis on melanthiaceae ensus late.";

"A phylogenetic analysis of the plastid matk gene with emphasis on melanthiaceae ensus late.";

"I the plast similar late.";

"I THOCHONDRIAL INTRONS.

"A PRAGIOUS PROMOMALY INTRONS.

"EMBL; AB040191; BAB16799.1; -..

"I THOCHONDRIAL INTRONS.

"EMBL; AB040191; BAB16799.1; -..

"I THOCHONDRIAL MATK N.

"A Pfam; PPO1448; Intron_maturas2; 1.

"Pfam; PPO148; Intron_maturas2; 1.

"M RNA processing; Chloroplast.

"M RNA processing; Chloroplast.

"M SEQUENCE 515 AA; 61780 MW; A4932FD7A8600BA8 CRC64;
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-i- FINCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY)
-i- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
EMBL, ABO40195; BAB1603.1; -.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR000464; MATUR.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01348; MATUR.).
MRNA processing; Chloroplast.
SEQUENCE S15 AA; 61945 MW; BBS0EOAR2DBDIF88 CRC64;
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Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;
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                                                                                                                                                          Score 40; DB 8; Length 515; Pred, No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                    1; Indels
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                              515 AA.
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                                                                                                                                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                        Intron maturase (Maturase K).
                                                                                                                                                            76.9%;
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                                                                                                                                                Query Match
Best Local Similarity 66...
6. Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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247 FLERIHFYV 255
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                                                                                                                                                                                                            1 FLHKVHFYV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=87628;
                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast
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Q9GHC5
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Q9GHD2
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Plant Biol. 2:415-427(2000).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                         Fuse S., Tamura M.N.; M. A. A. A. A. A. Diviogenetic analysis of the plastid matk gene with emphasis on Melathiaceae sensu late. ". Plant Biol. 2:415-427(2000).
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Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A phylogenetic analysis of the plastid matK gene with emphasis on Melanthiaceae sensu lato.";
                                                              Chloroplast.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01348; Intron_matúras2; 1.
Pfam; PF01344; MatK N; 1.
SEQUENCE SSING; Chloroplast.
SEQUENCE 515 AA; 61919 MW; 556C6A17A69204FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 24;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB040190; BAB16798.1; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MatK N.
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Intron maturase (Maturase K)
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tes 6; Conservative
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                                             Chionographis japonica.
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Fuse S., Tamura M.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FLHKVHFYV 9
                                                                                                                                       Chionographis.
NCBI_TaxID=119999;
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Melanthiaceae sensu lato.";

Lant Biol. 2:415-427(200).

C. !- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).

C. !- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,

AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY

MITOCHONDRIAL INTRONS.

DR FABL ABOLO991.1; -.

DR InterPro; IPR000442; Intron maturse2.

DR InterPro; IPR002866; Matk.N.

R Ffam; PP01346; Intron maturas2; 1.

RR Ffam; PP01346; Intron maturas2; 1.

RR Ffam; PP01934; Matk N; 1.

KW MRNA processing; Chloroplast.

SEQUENCE 515 AA; 61916 MN; 7EB6D08388182890 CRC64;
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;
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                                                                                                                                                                                                                                                                                                                                           76.9%; Score 40; DB 8; Length 515; 66.7%; Pred. No. 24; 1; Indels rative 1; Assmatches 1; Indels
                                                                                                                         EMBL; AB040193; BAB16801.1; -.
Interbro; IPR001443; Intron maturse2.
Interbro; IRR02866; Mark N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01844; Mark N; 1.
mRNA processing; Chloroplast.
SEQUENCE S15 AA; 61844 MW; 1BBFF413F5DE7848 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Intron maturase (Maturase K).
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Intron maturase (Maturase K).
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                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 66.73
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=87628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROUBLICE FROM N.A.

RAP Fuse S., Tamara M.N.;

Fuse S., Tamara M.N.;

Fuse S., Tamara M.N.;

RAP Fuse S., Tamara M.N.;

RAP Fuse S., Tamara M.N.;

RAP Fuse S. Tamara M.N.;

RAP Fuse S. Tamara M.N.;

RAP Fuse S. Tamara M.N.;

RE FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMILARITY)

C. 1- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMILARITY)

C. 1- SIMILARITY: MITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,

C. 2 SIMILARITY: BAB16795.1;

C. 3 SIMILARITY: BAB16795.1;

C. 3 SIMILARITY: BAB16795.1;

C. 4 SIMILARITY: MATURE C.

REL, AB040187; BAB16795.1;

REL, AB040182; MATK N.

REAM: PPO1348; Intron. matures2.

REAM: PROBABLY MATK N.

SW MRNA PROCESSING; Chloroplast.

SW SEQUENCE 515 AA; 61913 MW; 60674175DF2819DC CRC64;
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Fuse S., Tamura M.N.;
Fuse S., Tamura M.N.;
A phylogenetic analysis of the plastid matK gene with emphasis on Melanthiaceae sensu lato.";
Plant Biol. 2:415-427(2000).
-:- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Melanthiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
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              1; Indels
                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Intron maturase (Maturase K).
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              2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       Intron maturase (Maturase K).
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nes 6; Conservative
                 6; Conservative
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                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                            247 FLERIHFYV 255
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                                                                       1 FLHKVHFYV 9
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                    Matches
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247 FLERIHFYV 255
1 FLHKVHFYV 9
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01-OCT-2002
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"A phylogenetic analysis of the plastid matk gene with emphasis on melathiaceae sensu latto.";
Melathiaceae sensu latto.";
Plant Biol. 2:415-427(12000).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II INTRONS (BR SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
                                                                                                                                Fuse S., Tamura M.N.;

"A phylogenetic analysis of the plastid matk gene with emphasis on
"A phylogenetic analysis of the plastid matk gene with emphasis on
"A phylogenetic analysis of the plastid mate sensu late.";

Plant Biol. 2:415-427(2000).

-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).

-!- SIMILARITY: WITH CORRESPONDING ORP IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
                                   Chloroplast.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae,
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Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1: Todele
                                                                                                                                                                                                                                                                                                       Pfam; PF01348; Intron_matUras2; 1.
Pfam; PF01384; MatK N; 1.
Pfam; Processing; Chloropast.
SEQUENCE 515 AA; 61796 MW; 1C8FFF71CAF6CEF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515 AA; 61926 MW; FB689B0255959075 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Intron maturase (Maturase K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     515 AA.
                                                                                                                                                                                                                                                              EMBL; AB040185; BAB16793.2; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000442; Intron_maturse2.
Interpro; IPR002866; MatK_N.
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SEQUENCE 515 AA; 61926 MW;
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Best Local Similarity 66.77
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRIAL INTRONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FLHKVHFYV 9
                     rpsilandra thibetica.
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                                                                                          NCBI_TaxID=120020;
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SEQUENCE FROM N.A.
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PROTECTION OF TROM N.A.

PRUSE S., Tamura M.N.;

PRUSE S., Tamura M.N.;

PRUSE S., Tamura M.N.;

PRUSE S., Tamura M.N.;

Melanthiaceae sensu lato.";

Plant Biol, 2:415-477(2000).

I. Plant Biol, 2:415-477(2000).

I. PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMILARITY).

INTRONS (BY SIMILARITY).

AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.

RICHEPRO, IPROOMAGE, INTROM.

RICHEPRO, IPROOMAGE, INTROM MATURASE.

REPERFO, IPROOMAGE, INTROM MATURASE.

REPERFO, IPROOMAGE, INTROM MATURASE.

REPERFO, IPROOMAGE, INTROM MATURASE.

REPERFO, IPROOMAGE, INTROM MATURASE.

REPERFORM MATURASE.

REPERFO, IPROOMAGE, INTROM MATURASE.

REPERFORM FOLICE PROMACK N.

PEAM; PRO1814; MATK N.

PEAM; P
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Spermatophyta, Magnoliophyta, Liliopsida, Zingiberales, Zingiberaceae;
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                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Melanthiaceae, Chamaelirium.
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Kress W.J., Prince L.M., Williams K.J.,
"The phylogeny and a new classification of the gingers
(Zingibersecae): Bridence from molecular data.";
Am. J. Bot. 89:1684-1698(2002)
EMBL; AF478878; AAN63235.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515 AA; 62132 MW; 99BC93F9EB37635F CRC64;
                                                             (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
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PRT;
                                                                                                                                                                                   Intron maturase (Maturase K).
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Matches 6; Conservative
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=112831;
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SEQUENCE 5
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Query Match 76.9%; Score 40; DB 8; Length 515; Best Local Similarity 66.7%; Pred. No. 24; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps
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1 FLHKVHFYV 9 || ::|||| 247 FLERIHFYV 255 \$ q

Search completed: December 16, 2003, 14:17:59 Job time: 27 secs

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Human, cancer antigen, ATF4; CREB-2; vaccine, cytostatic;
immunogenic ligand; gene therapy; MHC; major histocompatibility complex;
adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cancer antigen ATP4/CREB-2 based immunogenic ligand #3
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                                                                                                                                 AAG19315
AAG40219
                                                                                                                                                                                                                                                                                             AAW20453
AAY41220
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AAB46370
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AAG76780
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         AAB40924
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31-MAY-2000; 2000US-209388P.
20-DEC-2000; 2000US-257007P.
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WO200192306-A2.
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 Human cancer antig
Human cancer antig
Novel human diagno
Simian immunodeffi
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Drosophila melanog
Drosophila melanog
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Prophenol oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                December 16, 2003, 14:06:05; Search time 33 Seconds (without alignments) 43.289 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                    A Geneseq 19Jun03:*

| SIDSIJgcgdata/geneseqp.embl/AA1980.DAT:*
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                                                                                                                                                                                                                                             1107863
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                             Notal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                   1107863 seqs, 158726573 residues
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                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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ABG19706
AAR10276
AAW56104
ABB59504
ABB57998
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AAW14441
                                                           OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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1 FLHKWHWVV 9
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Perfect score:
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88244444
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Arabioopsis thalia Novel human diagno H. pylori HELPY pr H. pylori HPC186 p H. pylori HPC186 p H. pylori Secreted Human colon cancer ORPI gene prod. in

Novel human secret Novel human diagno

Novel human diagno

Staphylococcus epi Drosophila melanog

Drosophila melanog Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Arabidopsis thalia

Arabidopsis thalia Arabidopsis thalia

Arabidopsis thalia

Polyglutamine-glut Human ORFX protein Human immune/haema

Gibberella fujîkur

M. leprae YY34-MYC Novel human diagno

Arabidopsis thalia Putative P. abyssi

Human peptidase-li

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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigon ATF4(FRB-2 (fort defined) and the polynuclectides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunohersepy comprising deministering to a subject the antibody, an immune effector cell that has been raised in vitro or in vivo in the presence and at the expense of an antigon presenting cell that presents the immunogenic compound in the context of an MTC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response of a context cell in gene therapy comprising administering an immune response of the synthetic and naturally occurring compounds. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for modulating an antibodies for the compounds are useful for immunotherapy when administered to a nitbodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polynucieotides are useful in diagnostic methods, for the detection and purification of antibodies. The present compounds are antigen and polynucieotides are useful in diagnostic methods, for the detection and purification of antibodies. The present compounds are antigen ATP4/CRBB-2 based immunogenic compounds and purification of antibodies. The present and purification of antibodies. The present and man cancer antigen ATP4/CRBB-2 based immunogenic compounds and purification of antibodies. The present antigen and purification of antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, cancer antigen, ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respective) but have not been cross-referenced or CDS features put in due to the degeneracy of the DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
New therapeutic compounds comprising immunogenic ligands, useful for
                     modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer antigen ATF4/CREB-2 based immunogenic ligand #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 61; DB 23; Length 9; 100.0%; Pred. No. 9.30+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                            Claim 3; Page 55; 69pp; English.
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20-DEC-2000; 2000US-257007P.
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen AFF4/CRBB-2 (not defined) and the polywacleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising that has administering to a subject the antibody, an immune effector cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response of context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response of the synthetic and naturally occurring compounds. The compounds are useful for modulating an immune response of the synthetic and naturally occurring compounds. The compounds are useful for treating cancer, particularly vaccines. The compounds are useful for treating cancer, particularly recognise and bind to these molecules. These antibodies are further useful for immunotherapy when administered to a castimodes are pecifically recognise and bind to these molecules. These antibodies are further useful for immunotherapy when administered to a castimunogens for the production and purification of antibodies, or as immunogens for the production of antibodies. The present income of the invention of a human cancer antigen ATF4/CREP-2 based immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respectively but have not been cross-referenced or CDS features put in due to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                      useful for
                                                                                 New therapeutic compounds comprising immunogenic ligands, useful modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degeneracy of the DNA sequences.
                                                                                                                                                                              Claim 4; Page 56; 68pp; English.
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                                        WPI; 2002-097764/13.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9 AA;
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Nicolette CA;
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Misc-difference 120
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                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in factivity. The polypeptide and polynucleotide sequences have applications in diagnostics, foremsics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AEG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

**Conditional Conditional Cond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                   Claim 20; SEQ ID No 50065; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIVmnd; HIV; AIDS; vaccine; pSMH103.
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hes 6; Conservative
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                               Drmanac RT, Liu C,
                                                           WPI; 2001-639362/73.
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(HYSE-) HYSEQ INC.
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                                                                              N-PSDB; AAS83893
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a vaccine
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                                                                                                                   SIV proteins may be produced from an E.coli expression system transformed with plasmid pSMH103. These may be used in diagnosis, treatment, and development of a vacagainst AIDS, as the sequence has the same structure as HIV-1 (but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, telomerase reverse transcriptase, hTRT, TRT, diagnosis, prognosis, cell proliferation, cancer, ageing, ribonucleoprotein.
New complementary DNA to RNA gene of simian immuno-deficiency virus - used for preparing vaccine and diagnosis agent for AIDS
                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                 68.9%; Score 42; DB 12; Length 172; 62.5%; Pred. No. 84; ive 2; Mismatches 1; Indels
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note= "encoded by TAA"
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note= "encoded by TAG"
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note= "encoded by TGA"
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note= "encoded by TGA"
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'note= "encoded by TAG"
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note= "encoded by TAG"
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note= "encoded by TAA"
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'note= "encoded by TAG"
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                                                                            Claim 2; Fig 4; 14pp; Japanese.
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                                                                                                                                                                                                                                   lacking the vpx gene).
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Misc-difference 4, Misc-differen	Misc-difference 5	PR-1998.  CT-1997; 9  UG-1997; 9  PR-1997; 9  PR-1997; 9  PR-1997; 9  PR-1997; 9  UG-1997; 9
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207 LHHWHW 212

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RESULT 7

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                Gaps
Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                             Score 42; DB 19; Length 587;
Pred. No. 2.7e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 5304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers EW;
                                                                                                                                                                                                                                                                          ABB59504 standard; Protein; 683 AA.
                                                                  Example 1; Fig 35; 387pp; English.
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                                                                                                68.9%;
55.6%;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                 FLHKWHWVV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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                                                                              Drosophila melanogaster polypeptide SEQ ID NO 786.
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ABB57998 standard; Protein; 684 AA
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                      Drosophila melanogaster.
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N-PSDB; ABL02101.
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wes 5, Conserv
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(ABB57737-ABB72072)
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                                                                                                                         pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                 interactions
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                            ABB57998;
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Gaps

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67.2%; Score 41; DB 22; Length 683; 83.3%; Pred. No. 4.3e+02; ive 0; Mismatches 1; Indels

Query Match 67.2 Best Local Similarity 83.3 Matches 5; Conservative

2 LHKWHW 7

95JP-0177444

13-JUL-1995;

us-09-870-089b-7.rag

Bombyx mori

Peptide Peptide Peptide Peptide

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This protein is a prophenol oxidase derived from a domestic silkworm. The phenol oxidase may be used as a novel labelling oxidase. The elucidation of the primary structure of the prophenol oxidase will contribute to the reconstitution of a prophenol oxidase activation which can be applied to the detection of microorganisms by measurement of beta-1,3-glucan and peptide glycan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                   (Pro)phenol oxidase derived from a domestic silkworm - useful as a labelling oxidase and in pro-phenol oxidase activation system for detection of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 18; Length 685;
Pred, No. 4.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen protein SEQ ID NO:4964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 6720; 9803pp; English.
                                                                                                                                                                                                     Claim 2; Page 14-17; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG74200 standard; Protein; 41 AA.
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                                                           LTD.
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03-NOV-1999; 99US-0163280.
                            95JP-0177444.
                                                           (WAKP ) WAKO PURE CHEM IND
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                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 83.3
Matches 5; Conservative
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                             13-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (Pro) phenol:oxidase from silkworm - useful as a labelling oxidase
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Silkworm; larvae; pro; phenoloxidase; Phe52-Val693; Phe52-Gly685
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                                                                                                                                                             /mote= "peptide fragment"
52..61
/note= "peptide fragment"
                                                                                                                "peptide fragment"
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/note= "claim 1"
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/label= pro-sequence
53..685
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                                                                                 Location/Qualifiers
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Best Local Similarity
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                        labelling oxidase
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Sequence

Matches

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AAW14441;

Protein Peptide

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therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing finactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell compared to the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAM37196 to AAM37204 and AAB37789 represent sequences used in the exemplification of the present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppessant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; attifungal; antirheumatic; antithyroid; antianted; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; sholester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; broom damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                            DB 22; Length 41; 42;
                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ORFX ORF688 polypeptide sequence SEQ ID NO:1376.
                                                                                                                                                                                                                                             Score 40; DB
Pred. No. 42;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            AAB40924 standard; Protein; 59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                             65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombosis; contraceptive
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-602362/57.
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Local 4; Conserve
                                                                                                                                                                                                                                                                                                                  || |:|::
27 LHPWNWII 34
                                                                                                                                                                                                                                                                                                  2 LHKWHWVV 9
                                                                                                                                                                                                                      41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAC75133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB40924;
                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                  AAB40924
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which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipordatic; antiparkinsonian; nootropic; neuropiccetive; onteopathic; antiporavisatic antianthat; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; untidiabetic; hypotensive; dermatological; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressave; antidiabetic; hypotensive; dermatological; immunosuppressave; antidiabetic; hypotensive; dermatological; immunosuppressave; antidiabetic; hypotensive; dermatological; immunosuppressave; antidiantency; and antidaneemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the proteins and nucleic acids way be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, grathematosus, severe combined immunodeficiency (SCID), AIDS, viral, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal heemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; mamme modulation; hamantopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; hamostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatheroselerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antibacterial; fungicide.
                                                                                                                                                                                                                             AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.6%; Score 40; DB 21; Length 59; 83.3%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human peptidase-like ORF54 protein, SEQ ID NO:108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                          Claim 11; Page 1172; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP31081 standard; Protein; 59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-2001; 2001WO-US17076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83...
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 LHGWHW 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LHKWHW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200190366-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP31081;
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Mycobacterium leprae.

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C designated ORF (open reading frame) 1-4534, and sequences ABM7504-
ABM79587 represent cDNAs encoding them. The invention also encompasses
C ABM79587 represent cDNAs encoding them. The invention also encompasses
C DOLYpeptides at least 80% identical to the ORF1-ORF434 (collectively)
C Februed to as ORFX) proteins, polymucleotides at least 85% identical to
C referred to as ORFX) proteins, polymucleotides at least 85% identical to
C polypeptides, methods of screening for modulators of ORFX proteins antibodies
C polypeptides, methods of screening individuals for a predisposition or
activity, and methods of screening individuals for a predisposition to an
ORFX-associated disorder. The ORFX proteins of the invention have a wide
C range of biological activities, such as cytokine, cell proliferation,
c range of biological activities, such as cytokine, cell proliferation,
c range of biological activity, hammen modulation, haematopoiesis regulation,
c range of biological activity, and may also be involved in the determination
c tissue growth, angiogenesis, activin or inhibin activity,
c elemokinheit activity, and may also be involved in the determination
c bodily characteristics, fertility and behaviour. ORFX proteins,
c chemokinheit and antibodies may be used in the treatment of cancers,
c other proliferation, disorders such as spoilapsy and Alzheimer's disease,
c other proliferation, disorders such as spoilapsy and Alzheimer's disease,
c other proliferation, disorders such as spoilapsy and Alzheimer's disease,
c other proliferation, disorders such as goowth and regeneration,
c storage disease, and infectious diseases caused by viral, bacterial,
c fungal and other pathogens.
C cradiovascular dispenses melliums, hypothyroidism, and cholesterol
c storage disease, and infectious diseases caused by viral, bacterial
c fungal and other pathogens.
C cradiovascular dispenses melliums, hypothyroidism, and other payents
c fungal and other proliferation and or or Respublic and an induction and or or reasoriate and probes, in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Membrane targeting protein; translocation protein; Escherichia coli;
Sec-independent pathway; protein transport; twin-arginine signal peptide;
mttABC operon; MttA protein.
                                                                                                                          Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                       ABP31028-ABP35561 represent 4534 novel human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.6%; Score 40; DB 23; Length 59; 83.3%; Pred. No. 59; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                               Claim 10; Page 297; 2508pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY41219 standard; Protein; 88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. leprae YY34-MYCLE protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                       Shimkets RA;
                                                                    WPI; 2002-106200/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHGWHW 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LHKWHW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 AA;
                                                                                         N-PSDB; ABN75107
                                                                                                                                                                                                       transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY41219;
                         Leach MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
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The invention relates to recombinant membrane targeting and translocation proteins from Escherichia coli. The recombinant relates to polypeptides are involved in the Sec-independent pathway for transport to proteins with a twin- arginine signal peptide to the periplasm or created lular medium and to the cell membrane. They transport fully folded and co-factor containing proteins. The polypeptides are used to transport such proteins, specifically to produce soluble forms of polypeptides that are normally produced in insoluble form. They may also be used to raise specific antibodies. Nucleic acid sequences that encode the polypeptides are used as probes to detect or isolate related genomic the polypeptides and humans. Producing normally insoluble proteins and their fragments and humans. Producing normally insoluble proteins in class, nematodes and humans. Producing normally insoluble proteins in class of the properly folded by cytoplasmic enzymes before translocation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                  New recombinant membrane targeting and translocation proteins from Bscherichia coli, used to produce soluble polypeptides normally produced in insoluble form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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0
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Pred. No. 86;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #513.
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                                                                                                                                                                                                                                                                                                                       Example 6; Fig 8; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 65.6%;
Local Similarity 75.0%;
les 6; Conservative 0
                                                                                         99WO-CA00272.
                                                                                                                      98US-0053197.
98US-0085761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-2002 (first entry)
                                                                                                                                                                                                 Turner RJ;
                                                                                                                                                                  (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                              WPI; 1999-633740/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSPWHWVV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LHKWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MttA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001.
                                                                                           29-MAR-1999;
                                                                                                                       01-APR-1998;
                                                                                                                                       28-MAY-1998;
                               W09951753-A1
                                                            14-OCT-1999
                                                                                                                                                                                                 Weiner JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG00522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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30-MAR-2001; 2001WO-US08631

99US-0121825

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990S-0138540.
990S-0138847.
990S-0139119.
990S-0139453.
990S-0139454.
990S-0139455.
990S-0139455.
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99US-0140695.
99US-0140823.
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99US-0139462.
99US-0139463.
99US-0139750.
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99US-0139817.
99US-0139899.
99US-0140353.
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99US-0141287.
99US-0141842.
99US-0142154.
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990S-0134218.
990S-0134219.
990S-0134221.
990S-0134370.
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99US-0135124.
99US-0135353.
99US-0135629.
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99US-0136782.
99US-0137222.
99US-0137528.
99US-0137502.
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99US-0132486.
99US-0132487.
99US-0132863.
                                                 990S-0126264.
990S-0126785.
990S-0127462.
990S-0128234.
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                                                                                                                                              99US-0130449
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                                                                                                                                                                                    99US-0131449
                                                                                                                                                                                                   99US-0132048
                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0136021
                        99US-0123548
99US-0125788
                                                                                                                                                                         99US-0130891
25-FEB-1999;

05-MAR-1999;

05-MAR-1999;

23-MAR-1999;

25-MAR-1999;

01-APR-1999;

06-APR-1999;

16-APR-1999;

16-APR-1999;

19-APR-1999;

13-APR-1999;

23-APR-1999;

23-APR-1999;

23-APR-1999;

30-APR-1999;

66-MAY-1999;

06-MAY-1999;

06-MAY-1999;

06-MAY-1999;
                                                                                                                                                                                                                                                                                            11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
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25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                   14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                             18-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-1999;
21-MAY-1999;
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18-JUN-1999
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18-JUN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN
  The invention relates to isolated polymucleotide (I) and polymerase chain reaction (FRR) primers, oligomers, and for chromosome polymerase chain reaction (FRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The conditions are also used in diagnostics as expressed sequence tags polymucleotides axer also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in companies for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Abd00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                             New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 15445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                  Claim 20; SEQ ID No 30881; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG15261 standard; Protein; 146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-2000; 2000EP-0301439.
                                                                                 Tang YT
                  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||:|||
44 IHKYHWV 50
                                                                                                          WPI; 2001-639362/73.
N-PSDB; AAS64709.
                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LHKWHWV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 123 AA;
                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1033405-A2.
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PR 04-007-1999; 99US-0115717.

PR 05-007-1999; 99US-0115765.

PR 06-007-1999; 99US-0115765.

PR 13-007-1999; 99US-0115765.

PR 13-007-1999; 99US-0118328.

PR 13-007-1999; 99US-0118328.

PR 13-007-1999; 99US-0118328.

PR 13-007-1999; 99US-0118328.

PR 14-007-1999; 99US-0118931.

PR 21-007-1999; 99US-0118931.

PR 21-007-1999; 99US-0118931.

PR 22-007-1999; 99US-0118931.
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Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

US-09-252-991A-28674
US-08-989-299-2
US-08-630-820-7
US-07-925-695-9
US-07-925-695-9
US-07-925-695-9
US-08-308-494A-13
US-09-134-001C-4203
US-09-134-001C-4203
US-09-134-001C-4203
US-09-134-001C-4203
US-09-134-001C-4203
US-09-138-3412-5
US-09-183-412-5
US-09-290-734-5
US-09-545-586-5
US-09-545-586-5
US-09-545-586-5

Appli Appli Appli Appli Appli Appli

Sequence

Sequence Sequence

Sequence Sequence Sequence

ALIGNMENTS

```
APPLICANT: Cech, Thomas R.
APPLICANT: Lighter, Joachim
APPLICANT: Lighter, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Mariley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: A COMPATIBLE
COMPUTER: FAM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Townsend and Townsend and Crew LLP 5 Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
APPLICATION DATA:
APPLICATION UNDRER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION WUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION WUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/854,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/974,549A
PALLING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/912 051
                                                                                                                                                                                                                                                                                                                                          Sequence 118, Application US/08974549A; Patent No. 6166178; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Two Embarcadero
683
8055
3033
3033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California
ADDRESSEE:
STREET: Two
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STATE:
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 Sequence 118, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 6, Appl
Sequence 615, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5382, Ap
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                                                                                            December 16, 2003, 14:11:00 ; Search time 12.3333 Seconds (without alignments) 30.875 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-974-549A-118
US-08-81-843A-4
US-08-81-08-34
US-09-183-19-14
US-09-083-19-14
US-09-083-19-14
US-09-083-19-14
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US-09-083-19-15
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US-09-19-63-19-63
US-09-19-63-18-85
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US-09-19-63-18-85
US-08-18-18-18-85
US-08-18-18-18-18
US-08-18-18-18-18
US-08-41-94-67
US-08-41-94-67
US-08-41-99
US-08-41-09-67
                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                  US-09-870-089B-7
61
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                            Copyright
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                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                             Scoring table:
                                                                         OM protein
                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
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Gaps
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION: 536
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: APDIE, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
                            US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                               01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.6
Matches 5; Conservative
         PRIOR APPLICATION DATA:
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23 FPHKWRWIL 31
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                            APPLICATION NUMBER: FILING DATE: 01-OCCLASSIFICATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-851-843A-4
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Pred. No. 3.2;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
CITY: San Francisco
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A FILING DATE: 06-MAY-1997
                                                                           FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: WO PCT/US97/17885.
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, Randolph Ted
REFERENCE/DOCKET NUMBER: 35,429
REFERENCE/DOCKET NUMBER: 35,429
REFERENCE/DOCKET NUMBER: 35,429
REFERENCE/DOCKET NUMBER: 35,429
REFERENCE/TON INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INPORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 08/844,419
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08851843A Patent No. 6093809 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.9%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.0
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE: 18-APR
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPHKWRWIL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FLHKWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-974-549A-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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US-09-053-197A-14
Sequence 14, Application US/09053197A
Sequence 14, Application US/09053197A
Sequence 11, Application US/09053197A
SENERAL INFORMATION:
APPLICANT: Weiner, Joel H.
APPLICANT: Weiner, Raymond J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN
TITLE OF INVENTION: SECRETION
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                68.9%; Score 42; DB 4; Length 552; 55.6%; Pred. No. 63;
                                                                                                                                                                                                                                                                       Indels
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Pred. No. 24;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                       2; Mismatches
                                 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-APR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
TELECOMMUNICATION INFORMATION:
TELEFRONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
COUNTRY: United States of America
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0
Lage 6; Conservative
                                                                                                                                                                                                                                                                       5; Conservative
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                                                                                                                                                                                                                                                                                                                                               23 FPHKWRWIL 31
                                                                                                                                                                                                                                                                                                             1 FLHKWHWVV 9
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                                                                                                                                                                                                                                                    Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-053-197A-14
                                                                                                                                                                                              US-09-430-323-4
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
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Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                     NAME: APPLE, RALIACLE.

REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 576-0200
TELEPX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-09-430-323-4
; Sequence 4, Application US/09430323
; Sequenc No. 6309867
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                 68.9%;
55.6%;
   FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T
                                                                                                                                                                                                                                                                                                                                                   Query Match 68.9
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                           TOPOLOGY: not releval
MOLECULE TYPE: protein
US-08-854-050-4
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ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REPERRICE/DOCKET NUMBER: UALB-03293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFRAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
                                                                                                                                                  Sequence 615, Application US/09732210 Patent No. 6573361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.9%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 HKWTWII 48
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CLASSIFICATION:
                                            48 EWHWVV 53
  4 KWHWVV 9
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Waigel, Detlef
APPLICANT: Salk Institute
TITLE OF INVENTION: FLOWERD PLANTS HAVING MODULATED FLOWER DEVELOPMENT
TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
FILE REPERENCE: SALKINS. 026A
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 1398-04-15
NUMBER OF SEQ ID NOS: 1398-04-15
SEQ ID NO 6
LENGTH: 104
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0
                                              GENERAL INFORMATION:
APPLICANT: Weiner, Joel H.
APPLICANT: Turner, Raymond J.
APPLICANT: Turner, Raymond J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN
TITLE OF INVENTION: SECRETION
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
STREET: California
COUNTRY: United States of America
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.9%; Score 39; DB 3; Length 104; 83.3%; Pred. No. 38; 1: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.6%; Score 40; DB 4; Length 88; 75.0%; Pred. No. 24; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,761A
FILING DATE: 28-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UALB-03356
TELEPOMNUMICATION INFORMATION:
TELEPOMNUMICATION INFORMATION:
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
TWANTON FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
Sequence 14, Application US/09085761A
Patent No. 6335178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09060726A Patent No. 6225530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LSPWHWWV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-060-726A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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FACENT NO. 80.73361

FACENT NO. 80.73361

APPLICANT: Bunkers, Greg J.

APPLICANT: Liang, Jihong

APPLICANT: Seale, Jeffrey W.

APPLICANT: Seale, Jeffrey W.

APPLICANT: Mittanck Cindy A.

APPLICANT: M. Younie S.

TITLE OF INVENTION: ALL: fungal Proteins and Methods for Their Use PILE REFERENCE: 38-21(15.08)B

CURRENT APPLICATION NUMBER: US/09/732,210

CURRENT APPLICATION NUMBER: US 60/169,513

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 1753

SEQ ID NO 615

LENGTH: 143

TYPE: PRT

ORGANISM: Methanococcus jannaschii
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Sequence 15. Application US/09053197A

BAPELICANT: Weiner, Joel H.

APPLICANT: THIER, RAYMONG J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN

TITLE OF INVENTION: SECRETION

NUMBER OF SEQUENCES:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 4; Length 143;
Pred. No. 51;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 01-APR-1998
CLASSIFICATION: 435
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Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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Redence 15, Application US/09085761A

Redence No. 6335178

GENERAL INFORMATION:
APPLICANT: Weiner, Joel H.
APPLICANT: Turner, Raymond J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTBIN TITLE OF INVENTION: SCREETION
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.3%; Score 38; DB 4; Length 79; 55.6%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 3; Length 79;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
CONTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTHARE: Patentl NElease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,761A
FILING DATE: 28 AMY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CATACOL, PEEF G.
REFIERRICE/OPOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/OPOCKET NUMBER: 32,837
TELECOMMUNICATION INFORMATION:
TELEPRANCE (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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US-08-411-768B-5
; Sequence 5, Application US/08411768B
; Patent No. 6083712
                                                                                                                                    ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-053-197A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not relevant
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
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Best Local Similarity 55.6
Matches 5; Conservative
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4 FTSIWHWVI 12
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                                                                                                                           amino acid
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US-09-085-761A-15
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                                              SEQUENCE CH
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Sequence 3486, Application US/09134001C

Sequence 3486, Application US/09134001C

Sequence 3486, Application US/09134001C

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 1998-08-13

FRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08
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APPLICANT: Olwen Birch
APPLICANT: Johann Brass
APPLICANT: Johann Brass
APPLICANT: Martin Fubramann
APPLICANT: Nicholas Shaw
TITLE OF INVENTION: Biotechnological Method
TITLE OF INVENTION: of Producing Biotin
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.3%; Score 38; DB 4; I
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATION SIGLED: FULLOS/FIGURED OF SOPTWARE: WordDerfect SOPTWARE: Version 5.1 CURRENT APPLICATION DATA: BAPLICATION NUMBER: US/08/411,768B FILING DATE: 31-March-95 CLASSIFICATION DATA: APPLICATION NUMBER: CH 3124/92 FILING DATE: 02-OCT-1992 PRIOR APPLICATION NUMBER: CH 2134/93 APPLICATION NUMBER: CH 2134/93
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                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 15-JUL-1993
INFORMATION FOR SEQ ID NO: 5:
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TYPE: amino acid
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MOLECULE TYPE: protein
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Rahme, Laurence
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                                                                                                                                                                                                                  APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA.

ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: ACII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERRICE/DOCKET NUMBER: 40,489
REFERRICE/TOX INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5382:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.7%; Score 37; DB 4; I 62.5%; Pred. No. 1.3e+02; vative 2; Mismatches 1;
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LOCATION: (B) LŌCATION 1...191
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SEQUENCE DESCRIPTION: SEQ ID NO: 5382:
US-09-107-532A-5382
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                                                                                                                                         US-09-107-532A-5382
; Sequence 5382, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Matches 5; Conservative
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52 LHQYHWYV 59
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167 LDRWHWI 173
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                         2 LHKWHWV 8
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                                                                                                                        RESULT 13
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Sequence 407, Application US/09199637A Patent No. 6355411 GENERAL INFORMATION: APPLICANT: Ausubel, Frederick APPLICANT: Goodman, Howard M.

RESULT 14 US-09-199-637A-407

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US-09-870-089B-7
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Sequence 9, Appli
Sequence 4, Appli
Sequence 21, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 754, Ap
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                                                                       ; Search time 22.1667 Seconds (without alignments) 75.512 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                     '(gm2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
'(gm2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
'(gm2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
'(gm2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
'(gm2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
'(gm2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
'(gm2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-870-089B-7
US-09-870-089B-9
US-09-843-676-4
US-09-766-223-4
US-10-053-758-4
US-10-053-758-4
US-10-054-611-4
US-10-054-611-4
US-10-106-698-4974
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US-09-870-089B-3
US-10-029-386-33052
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US-09-291-809C-8
US-09-845-849-8
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                           684280 segs, 185983659 residues
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                                                                         December 16, 2003, 14:18:11
                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                      Listing first 45 summaries
                                                 protein search, using sw model
                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
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115
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61
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98
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Perfect score:
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Maximum DB s
                                                  OM protein
                                                                                                                                                   Sequence:
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                                                                           Run on:
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No.
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Sequence 56, Appl
Sequence 1146, Appl
Sequence 1270, Appl
Sequence 72, Appl
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/870,089B; CURRENT FILING DATE: 2001-05-30; NUMBER OF SEQ ID NOS: 14
SOFTWARENT FILING DATE: 2001-05-30; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO?; LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Charles A. Nicolette
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REFERENCE: 68126881209900
CURRENT APPLICATION NUMBER: US/09/870,089B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
                                                        US-10-156 761-9146
US-10-156 761-9146
US-10-156-761-9120
US-10-130-912-72
US-10-140-018-72
US-10-140-912-72
US-10-140-922-72
US-10-140-922-72
US-10-140-922-72
US-10-140-92-72
US-10-141-92-72
US-10-141-702-72
US-10-141-702-72
US-10-141-702-72
US-10-141-702-72
US-10-142-432-72
US-10-142-432-72
US-10-142-432-72
US-10-143-994-72
US-10-145-431-72
US-10-145-628-72
US-10-145-631-72
US-10-145-831-72
US-10-145-831-72
US-10-145-831-72
US-10-145-831-72
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; Publication No. US20030175252A1
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0S-09-870-089B-7
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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Gaps

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Length 552;
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FILING DATE: 19-Jan-2001
CLASSIFICATION OF COMPACTION OF CASASTERIA PROPERTY OF COMPACTION OF COMPACTION OF CASASTERIA PROPERTY OF CASASTERIA OF 
                                                                                     Score 42; DB 10; Length 552;
Pred. No. 2.7e+02;
2; Mismatches 2; Indels
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Pred. No. 2.7e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471Alel Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09766253 Publication No. US20020187471A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morin, Gregg B.
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55.6%;
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                                                                                            68.9%;
55.6%;
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                            Query Match 68.9
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 FPHKWRWIL 31
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23 FPHKWRWIL 31
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Best Local Similarity
Matches 5; Conservat
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                   ;
US-09-843-676-4
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US-09-766-253-4
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Pred. No. 6.1e+05;
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APPLICANT: Cech, Thomas R.

Nakamura, Joachim
Nakamura, Toru
Chapaman, Karen B.

Morin, Gregg B.

Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. US20020164786Alel Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SVSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Prants Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 552 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20020164786A1 Relevant
TOPOLOGY: No. US20020164786A1 Relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 015389-002930US
CELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1197
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                               NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 576-0200
15) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09843676
Patent No. US20020164786Al
GENERAL INFORMATION:
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               2001-05-30
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       ; OTHER INFORMATION: ATF4/CREB-2 US-09-870-089B-9
                                                                                                                                                                                                                                                                                                                                                91.8%;
88.9%;
                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
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                   CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-843-676-4
                                                                                                            SEQ ID NO 9
LENGTH: 9
                                                                                                                                                                                                                                       FEATURE:
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Gaps

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Sequence 4, Application US/10053758 Publication No. US20030032075A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Б
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                                                                                                                           GENERAL INCOMMATION
GENERAL INCOMMATION
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019Alel Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCES: 223
CORRESPONDENCES: 223
CORRESPONDENCES: 223
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
CITY: San Francisco
CITY: San Francisco
COUNTEY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/438,486
FILING DATE: US/09/438,486
CLASSTERTANT AST
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
PILING DATE: 25-ARR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION WITHER: US 08/844,419
FILING DATE: 18-ARR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
FILING DATE: 01-0CT-1996
FILING DATE: 01-0CT-1996
ATOMORE: APPLICATION: 536
ATOMOREMENT ON PURPER: 015389-0029
REFISHATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
RECOMMUNICATION UNMBER: 015389-0029
TELECOMMUNICATION UNMBER: 015389-0029
TELECOMMUNICATION UNMBER: 015389-0029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 12-NOV-1999
CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAX-1997
CLASSIFICATION: 536
                                                      Sequence 4, Application US/09438486
Publication No. US2003009901941
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS: LENGTH: 552 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 FPHKWRWIL 31
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                                      -09-438-486-4
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RESULT 6 US-10-053-758-4

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APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chaman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        CUNTRY: California

CONTRY: United States of America
ZIP: 94111

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/854,050
PILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 11-APR-1996
ATTORNEY AGENT INFORMATION:

ATTORNEY AGENT INFORMATION:

ATTORNEY AGENT INFORMATION:

ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: No. US20030032075A1 Relevant
TOPOLOGY: No. US20030032075A1 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPERENCE/DOCKET NUMBER: 015389-002930US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KESULI,
10-104-295-4
; Sequence 4, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.;
; Inigner, Joachim
Nakamura, Toru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 552 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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Gaps
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                                                                                                                                                    COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown: 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
ATTORNEY/AGENT NUMBER: US 08/724,643
ATTORNEY/AGENT NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
ATTORNEY/AGENT NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REPERENDE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: STRANDENESS: NO: US20030059787A1 Relevant
TOPOLOGY: NO: US20030059787A1 Relevant
STREET: Two Embarcadero Center, 8th Floor
                                     CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein SEQ ID NO: 4: US-10-054-611-4
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Best Local Similarity 55.6
Matches 5; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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55.6%; Pred. No. 2.7e+02;
tive 2; Mismatches 2; Indels
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APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20030059787Alel Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:
                    Morin, Gregg B.
Harley, Calvin
Andrews, William H.

DF INVENTION: No. US20030044953Alel Telomerase
OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco CATTE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REPERRENENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION: TELEPHONE: (415) 576-0300
INFORMATION: TELEPHONE: (415) 576-0300
INFORMATION: (415) 576-0300
INFORMATION: (415) 576-0300
INFORMATION: CALL STANDOLOGY: No. 4:
TYPE: amino acids
TYPE: TYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US20030044953Al Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050
FILING DATE: cUnknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-10-054-611-4
Sequence 4, Application US/10054611
Publication No. US20030059787A1
                Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                       NUMBER OF INVENTION: NO. NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
TITLE REPERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-28
PRIOR PELICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,290
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: PAGENTIN VET. 3.0
SEPTION PAGENTIN VET. 3.0
SEQ ID NO 7554
LENGTH: 98
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NAME/KEY: MISC_FEATURE
LOCATION: (65)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) LOCATION: (98) 7
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-7554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (85) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equals any of the naturally occurring L-amino acids
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83.3%; Pred. No. 1.8e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-106-698-7554
Sequence 7554, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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                                                      50 EWHWVV 55
           4 KWHWVV 9
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APPLICANT: Burke, James
APPLICANT: Strittmater, Warren
APPLICANT: Nagai, Yoohitaka
TITLE OF INVENTION: COMPOUNS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
TITLE OF INVENTION: AND METHODS OF USE THEREOF
TITLE OF INVENTION: AND METHODS OF USE THEREOF
TITLE OF INVENTION: AND METHODS OF USE THEREOF
TITLE OF INVENTION: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/189,781
PRIOR PILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTION OF 21
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09291809C
; Sequence 8. Application US/09291809C
; Patent No. US20010049831A1
; GENERAL INFORMATION:
; APPLICANT: Balk Institute
; APPLICANT: Salk Institute
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; TITLE OF INVENTION: WODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; CURRENT APPLICATION NUMBER: US/09/291,809C
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: PCT/US99/08151
; PRIOR APPLICATION NUMBER: 09/060,726
; RRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 106
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; LOCATION: (37)
; CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4974
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                                                                                                  Query Match 65.6%; Score 40; DB 15; Length 41; Best Local Similarity 50.0%; Pred. No. 62; Matches 4; Conservative 3; Mismatches 1; Indels
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Pred. No. 29;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/09780070 Patent No. US20020009752A1
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US-09-291-809C-8
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80.0%;
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; ORGANISM: synthetic construct
US-09-780-070-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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27 LHPWNWII 34
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 4; Conserv
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Search completed: December 16, 2003, 14:41:06 Job time : 23.1667 secs
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Publication No. US20030194704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: PENN, DAVID R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 33052
LENGTH: 19
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US-009B-3
US-00-870-089B-3

Sequence 3, Application US/09870089B

Publication No. US20030175252A1

GENERAL INFORMATION:

APPLICANT: Charles A. Nicolette

TILLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER

TILLE REFERENCE: 68126881209900

CURRENT APPLICATION NUMBER: US/09/870,089B

CURRENT FILING DATE: 2001-05-30

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 3

LENGTH: 9

LENGTH: 9
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60.7%; Score 37; DB 12; Length 19;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:

OTHER INFORMATION: MAP TO Z49918.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.85

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91

US-10-029-386-33052
                        Ouery Match
62.3%; Score 38; DB 15; Length 98;
Best Local Similarity 55.6%; Pred. No. 2.38+02;
Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.7%; Score 37; DB 12; Length 9; Best Local Similarity 66.7%; Pred. No. 6.1e+05; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
CTHER INFORMATION: ATF4/CREB-2
US-09-870-089B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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FLQRWFWLV 13
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1 FLYKWHGFV 9
                                                                                                                        1 FLHKWHWVV 9
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4 VNKWHW 9
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US-10-029-386-33052
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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 16, 2003, 14:10:15 on: Run

; Search time 10.3333 Seconds (without alignments) 83.760 Million cell updates/sec

US-09-870-089B-7 Perfect score:

1 FLHKWHWVV 9 Seguence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

4:94 PIR ' Database :

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	conserved hypothet	conserved hypothet	vif protein - simi	thetical p		hypothetical prote	н	hypothetical prote		hypothetical prote	O	hypothetical prote	conserved hypothet	hypothetical prote	_		_	polyprotein - infe	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote		conserved hypothet	conserved hypothet	enterohemolysin 2	hypothetical prote		_
SUMMARIES	di i	₩.	G8278		F9587			E8707	G7517		T2892			C75311				T21891		H64559			C90735			: T36855		. A99775	Ω	AF2129
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hypothetical prote	probable membrane	sodium-dependent t	probable acid-CoA	probable exported	hemocyanin chain a	bromodomain protei	hypothetical prote	metal-regulated pr	hypothetical prote	hypothetical prote	apoptosis specific	hypothetical prote	replication-associ	aspartate dehydrog	aspartate dehydrog
F64022	S61598	D69902	G70604	AB0005	BHTLA	T49984	C90605	G69660	T29758	T49291	T40482	G64426	JC1418	E86621	G72002
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367	380	445	507	269	631	678	134	153	214	259	261	294	312	333	333
62.3	62.3	62.3	62.3	62.3	62.3	62.3	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7
38	38	38	38	38	38	38	37	37	37	37	37	37	37	37	37
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## ALIGNMENTS

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C. Species: Caulobacter crescentus
C. Species: Caulobacter crescentus
C. Species: Caulobacter crescentus
C. Species: Caulobacter crescentus
C. Species: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001
C. Accession: A87628
R. Mierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. A; Ecception Science Group et Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:2117369; PMIP:11259647

A;Modecule type: DNA A;Residues: 1-209 <STC> A;Cross-references: GB:AE005673; NID:g13424707; PIDN:AAK25021.1; GSPDB:GN00148 C;Genetics:

A;Gene: CC3059 C;Superfamily: Defnococcus radiodurans hypothetical protein DR1792

Gaps .. 0 Length 209; Indels . 75.4%; Score 46; DB 2; 71.4%; Pred. No. 3.9; tive 2; Mismatches Query Match Best Local Similarity 71.4 Matches 5; Conservative

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17 LHQWHWI 23 2 LHKWHWV 8 유

## RESULT 2

conserved hypothetical protein XF0597 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000

C;Accession: G82786
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenture 406, 151-157, 200
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G82086

A;Status: preliminary

A; Molecule type: DNA

A;Residues: 1-218 <SIM> A;Cross-references: GB:AE003905; GB:AE003849; NID:g9105456; PIDN:AAF83407.1; GSPDB:GNO

A:Experimental Bource: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fro)

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67.2%;
ilarity 62.5%;
Conservative
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128 LHRFHWIV 135
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A; Map position: 2
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J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa., R.G.; Santelli, R.V.; Sawabak A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.C.R.; da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, A.C.R.; da Silvai, A.
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-582 <KUR>
A;Cross-references: GB:ALS91985; PIDN:CAC48638.1; PID:g15140110; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
B;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
Bcience 293, 668-772, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Nov-1999
B;Acstarion: S;B080
A;Title: Sequence of a novel simian immunodeficiency virus from a wild-caught African ma;A;Accession: S28080; MUID:90015168; PMID:2797181
A;Accession: S28082
A;Status: nucleic acid sequence not shown; translation not shown
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A.Cross-references: GB:M27470; EMBL:X15781; NID:g334683; PIDN:AAB49570.1; PID:g334688
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1989
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C;Superfamily: Deinococcus radiodurans hypothetical protein DR1792
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A,Gene: vif
C,Superfamily: AIDS vif protein
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Tre-dependent RNA helicase [imported] - Arabidopsis thaliana CiSpecies Arabidopsis thaliana (mouse-ear cress) CiDate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 CiAccession: 684832 
A,Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A,Reference number: A96039; MUID:21368234; PMID:11474104
A,Contents: annotation
C,Genetics:
A,Gene: SMD:0248
A;Genome: plasmid
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C;Species: Mycobacterium leprae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 23-Mar-2001
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Pred. No. 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.6%; Score 40; DB 1; Length 88; 75.0%; Pred. No. 13; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Start codon: GTG
C,Superfamily: conserved hypothetical secreted protein HP0320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: EMBL:U00017; NID:g466994; PID:g467005
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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K;Smith, D.R.; Robison, K.
submitted to the EMBL Datary, November 1993
A;Description: Mycobacterium leprae cosmid B2126.
A;Reference number: S72585
A;Accession: S72850
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <SML>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
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Gaps ö

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A;Map position: 1
Tintrons: 43/2; 111/1; 185/3; 221/3; 298/2; 327/3; 364/2; 411/2; 500/1; 595/1; 643/3; 7
2; 1594/1; 1638/3
A;Molecule type: DNA
A;Residues: 1-295 «KMA»
A;Residues: 1-295 «KMA»
A;Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30720.1; PID:g3258037
A;Experimental source: strain OT3
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, April 1997
A, Description: The sequence of C. elegans cosmid C48B6.
A, Reference number: Z20544
A, Reference number: Z20544
A, Accession: T28923
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-1663 < MIN>
A, CROSS references: EMBL:U97189; PIDN: AAC48166.1; GSPDB:GN00019; CESP:C48B6.6
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28923
                                                                                                                                                                                                                              2; Length 295;
                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C48B6.6 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - Methanococcus jannaschii
                                                                                                                                                                                                                              Score 40; DB
Pred. No. 44;
                                                                                                                                                                                                                                                                                   0; Mismatches
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C;Superfamily: rat ribosomal protein L27a
                                                                                                                                                                                                                           Query Match 65.6%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.6
Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 FIEKWDWII 83
                                                                                                                                                                                                                                                                                                                                                                                                  86 FFHKWSW 92
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                                                                                                                                                                                                                                                                                                                                          1 FLHKWHW 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ribosomal protein L15
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                                                                                                                                                                                                                                                                                Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: E87075

A;Accession: preliminary

A;Molecule type: DNA

A;Residues: 1-95 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . ------- t--cov <raw>
A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49478.1; PID:g545798
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein PH160B - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: H71039
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfu:u, Y.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A)Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                     R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
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                                                                                       C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C;Accession: E87075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein PAB1992 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: ML1331
C;Superfamily: conserved hypothetical secreted protein HP0320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 2;
Pred. No. 39;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.6%; Score 40; DB 2; 75.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Best Local Similarity 71.4%;
Matches 5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LHKWHWVV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: G75174
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Cipecies: Methanococcus jannaschii.
Cipecies: Methanococcus jannaschii.
Cipecies: Methanococcus jannaschii.
Cipate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
Cipate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
Cipacession: E64359
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R. Reich, C.J.; White, O.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Fran, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Reference number: A64300; MUD:96337999; PMID:8688087
A;Accession: E64359
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                                                                                                    Gaps
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0
65.6%; Score 40; DB 2; Length 1663; 44.4%; Pred. No. 2.5e+02; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.9%; Score 39; DB 2; Length 143; Best Local Similarity 57.1%; Pred. No. 31; Matches 4; Conservative 2; Mismatches 1; Indels
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Search completed: December 16, 2003, 14:19:16
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Conservative
                                         11 VHPWHWWV 18
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2 LHKWHWVV 9
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nes 5; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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Kunst, F.; Ogaswara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
Kunst, F.; Ogaswara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

; Enrisch, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

; Enrisch, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

; Enrisch, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

; Authors: Foulger D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

sch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

sch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Furine, A.; Hosono, S.; Hullo, M.F.

sch, J.; Koningstein, G.; Kroda, E.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Ervine, A.; Liu, H.; Masuda, S.; Mausel,

; Authors: Lauber, J.; Lazarevic, W.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron,

; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron,

; Authors: Schleich, S.; Schroeter, R.; Yosmane, K.; Yasuano,

; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.;

; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

; Reference number: Ac9580; MUID:98044033; PMID:9384377
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K,White, O., Elsen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
Science 286, 1571-1577, 1999
A;Ritle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Status: preliminary
A; Modecule type: DNA
A; Reaidues: 1-159 < WHI>
A; Cross-references: GB: AE002048; GB: AE000513; NID: g6459929; PIDN: AAF11686.1; PID: g645993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .Residues: 1-145 < KUN>
).Cross-references: GB:Z99120, GB:AL009126; NID:g2635613, PIDN:CAB15183.1; PID:g2635690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,Accession: A70014
.,Status: preliminary; nucleic acid sequence not shown; translation not shown
.,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C,Species: Deinococcus radiodurans
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                          pothetical protein yukd - Bacillus subtilis
Species: Bacillus subtilis
Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 63.9%; Score 39; DB 2; Length 145; Local Similarity 66.7%; Pred. No. 31; length 145, les 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1, Superfamily: Bacillus subtilis hypothetical protein yukd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches 5; Conserva
                                                                                                         42 HKWTWII 48
                                     3 HKWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KWHWIM 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1
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Cjāccession: AG2462
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yamada, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                               C,Accession: T06656
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15791
A;Accession: T06656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein al15255 [imported] - Nostoc sp. (strain PCC 7120) C.Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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A;Experimental source: strain PCC 7120
hyporhetical protein T6G15.90 - Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AL049656; GSPDB:GN00062; ATSP:T6G15.90
A;Experimental source: cultivar Columbia; BAC clone T6G15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.9%; Score 39; DB 2; Length 210; 71.4%; Pred. No. 45; tive 1; Mismatches 1; Indels
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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 16, 2003, 14:06:35; Search time 5.6667 Seconds (without alignments) 74.689 Million cell updates/sec Run on:

US-09-870-089B-7 61 1 FLHKWHWVV 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		,			SUMMAKIES	
1		<b>*</b>				
No.	Score	Match	Length	DB	ID	Description
1	42		172	-	VIF SIVGB	P22383 simian immu
7	40	9:59	88	Н	TATA MYCLE	P54079 mycobacteri
m	39	63.8	143	Ч	RL15 METJA	P54047 methanococc
4	39	63.9	310	Н	Y160_BUCAP	Q8k9x4 buchnera ap
Ŋ	39	63.8	360	ч	IL8B_BOVIN	bos tauru
9	39	63.9	529	Ч	C6T1_DROME	
7	38	62.3	79	٦	TATA HELPJ	Q9zmb8 helicobacte
∞	38	62.3	79	ч	TATA HELPY	
6	38	62.3	158	m	YBHB_ECOLI	P12994 escherichia
	. 38	62.3	179	Н	YH94_STRCO	Q9x9z8 streptomyce
	38	62.3	367	щ	YC36 HAEIN	
	38	62.3	380	н	COSC YEAST	
13	38	62.3	628	Н	HCYC_EURCA	
	38	62.3	630	Н	HCYA_EURCA	
	37	60.7	138	Н	YB27_HAEIN	
16	37	60.7	153	Н		
	37	60.7	339	٦	SPSG_BACSU	
18	37	60.7	389	Н	ALKB_HUMAN	Q13686 homo sapien
19	37	60.7	623	н	HCYE_EURCA	
20	37	60.7	626	Н	HCY6_ANDAU	
21	37	60.7	626	Н	HCYB_EURCA	
22	37	60.7	626	Н	HCYD_EURCA	eurypeln
23	37	60.7	628	٦	HCY2_LIMPO	
24	37	60.7	628	Н.	HCYF_EURCA	eurypel
25	37	60.7	965	Н	PSD1_CAEEL	
26	37	60.7	1002	Н	- 1	_
27	36.5	59.8	220	Н	NADD_YERPE	
28	Ġ	59.8	5596	7		homo sapi
29	36	59.0	144	Н		baci
30		59.0	4	Н	- 1	Q43953 azotobacter
31	36	59.0	4	Н	CYBH_AZOVI	P23000 azotobacter
32	36	59.0	299	Н		Q01109 streptomyce
33	36	59.0	φ	ч	YCX7_ODOSI	

See   PAP SCHPO   Q10295 schizosacch   CATA_ERYGR   Q9x1p0 erysiphe gr   Q9x1p0 erysiphe gr	OARD; PRT; 172 AA. , Created) , Last sequence update) , Last annotation update) ; actor (SOR protein).	Vir. Simian immunodeficiency virus (isolate GB1). Viruses; Retroid viruses; Retroviridae; Lentivirus. Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TAXID=11732; [1] SEQUENCE FROM N.A. MEDLINE=90015168; PubMed=2797181; MEDLINE=90015168; PubMed=2797181; MEDLINE=90015168; PubMed=2797181; MEDLINE=90015168; PubMed=2797181; MEDLINE=90015168; PubMed=2797181; MEDLINE=90015168; PubMed=2797181; Noorigan E.W., Moriyama E.M., Golobori T., Hayami M.; Sequence of a novel simian immunodeficiency virus from a wild-caught African mandrill.; Nature 341:539-541(1989)	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of BioInformatics and the EMBL outstation the Buropean Bioinformatics Institution. There are no restrictions on it use by non-profit institutions along as its content is in no war modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license agreement (See http://www.isb-sib.ch/announce EMBL, MZTATO, AMB4957.1;	68.9%; Score 42; DB 1; Length 172; 62.5%; Pred. No. 8.6; ttive 2; Mismatches 1; Indels	DARD; PRT; 88 AA. t, Created) t, Last sequence update) t, Last annotation update) t, Last annotation update) edin translocase protein tatA/E homolog.
566 719 719 971 1018 3033 116 115 154	E v v B	viruses; viruses;	nntry is in Instit in instit is stateme is a licer to lic	68 62 itiv	ANDARD; 34, Cr 34, Le 41, Le
88888888888888888888888888888888888888	ST (Rel. (Rel. (Rel.	immunodefi xID=11732; xID=11732; E FROM N.A. =90015168; H.W., Mori ce of a no mandrill. mandrill. imandrill.	PROT en e Swisss n Bioin n-profi duires email to 0; AAB4 PRO0047 59; Vif 0349; V	Stmilarity f; Conserva 2 LHKWHWVV 9 1 EKWHWLV 26	(Re (Re (Re
4 W 7 C 88 Q O T 1 G W 4 R W W M W M M M M M M M M M M M M M M M	E_SIVGB VIF_SIVGB VIF_SIVGB P22383; 01-AUG-1991 (Rel. 15 01-AUG-1991 (Rel. 15 01-AUG-1991 (Rel. 17 Virion infectivity in	Vir. Simian immunodefi Viruses; Retroid Viruses; Retroid NCBI_TaxID=11732; GIOIENCE FROM N.A MEDLINE=90015168; TSUJIMOLO H., Has COOPER R.W., MORI "Sequence of a no African mandrill. Nature 341:539-54 -i- FUNCTION: DET	This SWISS-PROT entry is between the Swiss Institute the European Biointo-institute by non-profit in modified and this statementities requires a lice or send an email to lice send. The PROSESS, Vig. 1.  PRINTS; PRO0559; Vig. 1.  PRINTS; PRO0055; Vig. 1.  PRINTS; PRO0055; Vig. 1.  PRINTS; PRO0056; Viral AINS.  SEQUENCE 1/2 AA; 204;	Query Match Best Local 9fm Matches 5; 7 2 LH 7 19 IE	RESULT 2  TATA_MYCLE  ID TATA_MYCLE  AC P44079;  DT 01-0CT-1996 (Re- DT 01-0CT-1996 (Re- DT 28-FEB-2003 (Re- DE Sec-independent
W W W W W A A A A A A A N O C B O O O O O O	RESULT VIF SI ID P AC AC DT OT	000844446000		Oue Bes Matr Oy Db	RESULTITATA I

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                                                                                                                                              SEQUENCE FROM N.A.

STRAIR=JAL-1 / DSM 2661 / ATCC 43067;

STRAIR=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=868087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Scotton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22084549; PubMed=12089438; Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S., Tamas I., Klasson L., Canbaeck B., Marian N.A., Andersson S.G.E.; Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; 50 million years of genomic stasis in endosymbiotic bacteria."; Science 296:2376-2379(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.9%; Score 39; DB 1; Length 143; Best Local Similarity 57.1%; Pred. No. 20; Matches 4; Conservative 2; Mismatches 1; Indels
                        Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribosomal protein; Complete proteome.
SEQUENCE 143 AA; 16107 MW; 2A78A8ABA578FF87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein BUsg160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; MJ0477; -.
INTERPO: INTERPO! TREADSOMAL_LIS.
PETAN, PRO0256; LIS; 1.
PROSITE; PSO0475; RIBOSOMAL_LIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U67497; AAB98466.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; E64359; E64359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 HKWTWII 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 HKWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=98794;
  RPL15P OR MJ0477
                                                                                                      NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BUCAP
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ID Y160_BUCA
AC Q8K9X4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BUSG160.
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                                                                                                                                                                                                                                                                                  STRAIN=TN;

MREDLINSE=21128732; PubMed=11234002;

Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

Barreil B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: REQUIRED FOR CORRECT LOCALIZATION OF PRECURSOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; ALO35310; CAA22941.1; -.
EMBL; ALO35310; CAA22941.1; -.
EMBL; ALS83921; CAC31712.1; ALT_INIT.
Leproma, ML1331; -.
HAMAP; MF 00236; -; -.
HAMAP; MF 00236; -; -.
HAMAP; MF 00236; -; -.
InterPro; IPR006312; TatA_E.
Pfam; PF02416; MtA_HCf106.
ITGREPAM; TGR0411; tatA_E; 1.
TIGREPAM; TGR0411; tatA_E; 1.
Transport; Protein transport; Translocation; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1; Length 88; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                    Smith D.R., Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
OR ML1331 OR MLCB2533.27 OR U2126B OR B2126_C1_182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Membrane-bound (Probable). SIMILARITY: BELONGS TO THE TATA/E FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97F8C81009F7CAC8 CRC64;
                                                                   Corynebacterineae, Mycobacteriaceae, Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 50S ribosomal protein L15P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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01-OCT-1996 (Rel. 34, Last seqn
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 AA; 9824 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U00017; AAA17190.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHKWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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P54047;
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RESULT 3
RL15\_METJA
ID RL15\_ME
AC P54047;
DT 01-OCTDT 16-OCTDE 50S rib

**Matches** 

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Gaps

0

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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Li Y., Feng J., Templeton J.W.;

Li Y., Feng J., Templeton J.W.;

Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL.

- REUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY (BY
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                   63.9%; Score 39; DB 1; Length 310; 66.7%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last amontation update)
High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U19947; AAA84996.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCREHDDOPSN.
PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS050262; G_PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                            InterPro; IPR005496; TerC.
Pfam; PF03741; TerC; 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                      POTENTIAL.
44B75CDED6B47004 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 AA
                                                                                                                                                                                                                                                                                                                                                   Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                         POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                              EMBL; AE014091; AAM67728.1; -.
                                                                                                                                                                                                                                                                                                       36938 MW;
                                                                                                                                                                                                                                                                                                                                                     66.78;
                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                         228
256
284
310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 132 KWHWIL 137
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   4 KWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
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Q28003;
                                                                                                                                                                             TRANSMEM
TRANSMEM
TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                        SEQUENCE
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RC STRAIN=Berkeley,

RX Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Holt R.W., Hoskins R.A., Galle R.E.,

RA Amanatides P.G., Scherer S.E., Holt R.W., Hoskins R.A., Galle R.E.,

RA Amanatides P.G., Scherer S.E., Holt W., Hoskins R.A., Galle R.E.,

RA Briton G.G., Wortenan J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej K.G., Change M., Pfeiffer B.D.,

RA Briton G.G., Wortenan J.R., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basun A., Baxendale J., Bayraktaroglu L., Besaley B.M.,

Ballew R.M., Basun A., Baxendale J., Bayraktaroglu L., Besaley E.M.,

RA Ballew R.M., Buck J., Bouck J., Brotkern P., Bolshakov S.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Borkova D., Botcher A., Deng Z., Mays A.D., Daw, I., Dister S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Borsin C., Mabrielian A.E., Garg N.S., Gelbart W., Glaschmann M.,

RA Boster C., Gabrielian A.E., Garg N.S., Gelbart W.A., Ketchum K.A.,

RA Harris N.L., Harvey D., Heiman T.J., Werniandez J.R., Houck J.,

RA Harris N.L., Heily W., Mowland T.J., Wei M.H., Ibegwam C.,

RA Jalai M., Kalush F., Karpen G.H., Kez, Kennison J.A.,

Rimmel B.E., Kodira C.D., Krafer G., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Lei Y., Mowland T.J., Wei M.P.,

Rasko P., Lei Y., Mowland T.J., Wei M.P.,

Ra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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0
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.9%; Score 39; DB 1; Length 360; 100.0%; Pred. No. 47; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                          -LINKED (GLCNAC. . .) (PC 9A7F70C982A632D1 CRC64;
                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cytochrome P450 6t1 (EC 1.14.-.-) (CYPVIT1).
CYP6T1 OR CG1644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529 AA
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                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                             CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                  316
119
10
24
360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 KWHWV
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Chemotaxis.
DOMAIN
                                                                                         TRANSMEM
DOMAIN
                                                                                                                                                             DOMAIN
TRANSMEM
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TRANSMEM
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                                             RANSMEM
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Nature 397:176-180(1999)
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Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skrong R., Sun E.,
Nang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J. S., Zhan M., Zhang G., Zheng I.,
Zheng X.H., Zhong F.N., Zhong W., Zhan G., Zhao Q., Zheng I.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000)
C.!- FUNCTION: MAY BE INVOLUED IN THE METABOLISM OF INSECT HORMONES AND
IN THE BREAKDOWN OF SYMTHETIC INSECTICIBES (BY SIMILARITY)
C.!- CATALITYTC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
C.!- CATALILAR LOCATION: Membrane-bound. Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003568; AAF50807.1; -.
HSSP; P14779; 1JPZ.
HSSP; P14779; 1JPZ.
HSSP; P14779; 1JPZ.
INCHEPPO; IPRO011182; Cyp6t1.
PFIAME; PRO067; p450; 1.
PRINTS; PRO0085; P450; 1.
PROSTITE; PRO0086; CYTOCHROME P450; 1.
Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
Endoplasmic reticulum; Hyporhetical procein.
METAL
H72 472
H72 H72 IRON (HEMB AXIAL LIGAND) (BY SIMILARITY).
SEQUENCE 529 AA; 60518 MW; 2BAD7875F3BD9C10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso B., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter \operatorname{pylori."};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Sec-independent protein translocase protein tatA/E homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.9%; Score 39; DB 1; Length 529; 83.3%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99120557; PubMed=9923682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 LHFWHW 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATA OR JHP0303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATA HELPJ
09ZMB8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
TATA_HELPJ
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
-!- FUNCTION: REQUIRED FOR CORRECT LOCALIZATION OF PRECURSOR PROTEINS
BEARING SIGNAL PEPTIDES WITH THE TWIN ARGININE CONSERVED MOTIF
S/T-R-R-X-F-L-K. THIS SEC-INDEPENDENT PATHWAY IS TERMED TAT FOR
TWIN-ARGININE TRANSLOCATION SYSTEM. THIS SYSTEM MAINLY TRANSPORTS
PROTEINS WITH BOUND COFACTORS THAT REQUIRE FOLDING PRIOR TO EXPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pylori.",
Nature 388:539-547 (1997).
Nature 388:539-547 (1997).
PRECURSOR PROTEINS
BEARING SIGNAL PEPTIDES WITH THE TWIN ARGININE CONSERVED MOTIF
S/T-R-R-X-F-L-K. THIS SEC-INDEPENDENT PATHWAY IS TERRED TAT FOR
TWIN-ARGININE TRANSLOCATION SYSTEM THIS SYSTEM MAINLY TRANSPORTS
PROTEINS WITH BOUND COPACTORS THAT REQUIRE FOLDING PRIOR TO EXPORT
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SETAIN=26655 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlawage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Pujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Helicobacteraceae, Helicobacter.
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PIR; A71948; A71948.
HAMAP; MF 00236; -; 1.
InterPro; IPR005312; TatA_E.
Pfam; PR0415; MttA_HCf106.
ITGRFAMS; TIGR011; LATA_E.
TIGRFAMS; TIGR011; LATA_E.
Transport; Protein transport; Transhorane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Sec-independent protein translocase protein tatA/E homolog.
TATA OR HP0320.
                                                                                                                                                                                        (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Inner-membrane bound (Probable).
-!- SIMILARITY: BELONGS TO THE TATA/E FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 AA; 8752 MW; D39E9DCA02AA5E8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.3%; Score 38; DB 1; 55.6%; Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATA HELPY
025088;
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-i- SUBUNIT: Homodimer.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE UPF0098 FAMILY.
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30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical protein SCO1794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 AA.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                        Ecodene; Ed11238; ybhB.
LiterPro; IPR001247; Cons_hypoth481.
InterPro; IPR001858; PBP.
Pfam, PF01161; PBP; ITGR00481; ITGRR0481; ITGRR0481; ITGR00481; I.
3D-structure; Complete proteome.
COMPLICT 136 G -> A (I
                                                                                                                                                                                                                                                                                                                                               EMBL, AE000180, AAC73860.1; -. PIR, E64813, Q3ECBA.
PDB; 1FJJ; 18-JUL-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.3%; 8
                                                                                                                                                                                                                                                                                                                      EMBL; J04423; AAA23513.1; -.
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147
158 AA;
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE
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YH94 STRCO
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDILINE=89066784; PubMed=3058702;
MEDILINE=89066784; PubMed=3058702;
Octsuka A.J., Buoncristiani M.R., Howard P.K., Flamm J., Johnson O.,
Yamamoto R., Uchida K., Cook C., Ruppert J., Matsuzaki J.;
"The Bscherichia Cali biotin biosynthetic enzyme sequences predicted
from the nucleodide sequence of the bio operon.";
J. Biol. Chem. 263:19577-19585 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21332775; PubMed=11439028;
Serre L., Pereira de Jesus K., Zelwer C., Bureaud N., Schoentgen F.,
Benedetti H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                          PIR; H64559; H64559.

TIGR; HP0320; --
HAMAP; MF 00236; --; 1.

InterPro; IPR0053369; MttA Hcf106.

InterPro; IPR005312; TatA E.

Pfam; PF02416; MttA Hcf106, 1.

TIGRFAMs; TIGR011; tatAB; 1.

TIGRFAMs; TIGR011; tatAB; 1.

Transport; Protein transport; Transmembrane;
                      SUBCELLULAR LOCATION: Inner-membrane bound (Probable). SIMILARITY: BELONGS TO THE TATA/E FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose
Mau B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 1; Length 79;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CES99ACA02AASE8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P12994; P75766;
01-JAN-1990 (Rel. 13, Created)
N-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane; Complete proteome
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                                                                                                                                                                                                                                                                                                                    EMBL; AE000550; AAD07397.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 AA; 8722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.v.,
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISIWHWVI 12
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  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein ybhB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YBHB ECOLI
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  SO THE WAR WAR WAS A STANDARD TO THE SOUTH OF THE SOUTH O
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G -> A (IN REF. 1).
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31;
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258 ;
380 AA;
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                                                                                                                                                                                                                                                                                                                                   4 KWHWV 8
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                                                                                                                                                                                                                                                                                                                                                                                                                               COSC YEAST
P53053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                               MEDLINE-21996410; PubMed=12000953; MEDLINE-21996410; PubMed=12000953; MEDLINE-21996410; PubMed=12000953; Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kleser H., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Karlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICRFAMS; TIGR00481; TIGR00481; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 179 Aa; 19158 MW; AC4A6A43BD830861 CRC64;
 Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.3%; Score 38; DB 1;
100.0%; Pred. No. 34;
ive 0; Mismatches
                                                                                                                                                                                                                     coelicolor A3(2).";
Nature 417:141-147(2002).
-!- SIMILARITY: BELONGS TO THE UPF0098 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 AA
                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Son sand an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AL939110; CAB45286.1; -.
PIR, T36855, T36855.
HSSP, P77368; IFUX.
INTERPRO, IPRO05247; CONS_hypoth481.
InterPro; IPRO01858; PBP.
Pfam; PF01161; PBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein HI1236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae.
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Best Local Similarity
                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 WHWVV 9
                                                                                                                                                                                           Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YC36 HAEIN
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"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast 12:1555-1562[1996].
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE DUP/COS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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STRAIN=S288C / FY1679;
MEDLINE=97127827; PubMed=8972578;
Coissac E., Maillier E., Robineau S., Netter P.;
"Sequence of a 39,411 bp DNA fragment covering the left end of chromosome VII of Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.3%; Score 38; DB 1; Length 367;
80.0%; Pred. No. 67;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; H11236; -. Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 AA; 41355 MW; B00211C5F98C2585 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
52F58F4E400CA596 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                Science 269:496-512(1995).
-!- SIMILARITY: TO E.COLI YDGA AND YIHF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44803 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U32803; AAC22888.1; -. PIR; F64022; F64022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X94357; CAA64124.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, Z72785; CAA96983.1; -. PIR, S61598, S61598. SGD; S0003232; COS12. InterPro; IPR001142; DUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COS12 protein.
COS12 OR YGL263W OR NRC380.
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DER REPRESENTATION OF THE PROPERTY OF THE PROP
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MEDLINE=20564303; PubMed=10961996;
MEDLINE=20564303; PubMed=10, Schweikardt T., Decker H., Burmester T.;
Voit R., Feldmaier-Fuchs G., Schweikardt T., Decker H., Burmester T.;
"Complete sequence of the 24-mer hemocyanin of the tarantula Eurypelma californicum. Structure and intramolecular evolution of the
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Subunits.";
J. Biol. Chem. 275:39339-39344(2000).
J. Biol. Chem. 275:39339-39344(2000).
-!- FUNCTION: HEWOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY WOLLUSKS AND OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF WATH SEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARTHROPODS.
-!-SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFED.
-!-SUBCELLULAR LOCATION: Extracellular.
-!-TISSUE SPECIFICITY: Hemolymph.
-!-TISSUE SPECIFICITY: Hemolymph.
-!-IGANDS (PRESUMABLY CONPER IONS BOUND EACH HAVE 3 NITROGEN LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.
-!-SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eurypelma californica (American tarantula).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Mygalomorphae, Theraphosidae, Aphonopelma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Copper; Glycoprotein; Hemolymph.
BY SIMILARITY.
BY SIMILARITY.
COPPER 1 (BY SIMILARITY).
COPPER 1 (BY SIMILARITY).
COPPER 1 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
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Score 38; DB 1; Length 380;
Pred. No. 69;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000896; Hemocyanin.
InterPro; IPR005203; hemocyanin C.
InterPro; IPR005204; hemocyanin N.
InterPro; IPR00227; Tyrosinase.
Pfam; PF0372; hemocyanin; 1.
Pfam; PF0372; hemocyanin, 1.
Pfam; PF0372; hemocyanin N; 1.
PROSITE; PS00209; HEMOCYANIN 1; 1.
PROSITE; PS00210; HEMOCYANIN 1; 1.
PROSITE; PS00498; TYROSINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ277489; CAB89495.1; -.
      62.3%;
80.0%;
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                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                              STANDARD;
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         Query Match
Best Local Similarity
                                                                                                                                                                   194 KWHWI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iransport; Oxygen
INIT_MET 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=29932;
                                                                                                                               4 KWHWV 8
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178
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                 HCYC EURCA
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METAL
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                                                                                                                                                                                                                                                                               RESULT 13
HCYC EURCA
AC CONTCO
DT 28-FEBB
DT
                                                              Matches
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                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 91025623; PubMed=2222854; Schartau W., Metzger W., Sonner P., Geisert H., Storz H.; Schartau W., Metzger W., Sonner P., Geisert H., Storz H.; Schartau W., Etger W., Sonner P., Geisert H., Storz H.; Schartan Endocyanins in spiders, XXIII. Complete amino-acid sequence of subunit a of Eurypelma californicum hemocyanin."; Biol. Chem. Hoppe-Seyler 371:557-565 (1990).
-!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTHEORDE.

-I-SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN
DIFFERENT CHAINS IDENTIFIED.
-I-SUBCELLULAR LOCATION: Extracellular.
-I-SUBSUE SPECIFICITY: Hemolymph.
-I-MISCELLANBOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN
LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A
BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN
ADDITION TO BINDING OXYGEN.
-I-SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
MEDLINE=91060544; PubMed=2246235;
MODLINE=91060544; PubMed=2246235;
Wort R., Feldmaier-Fuchs G.
"Arthropod hemocyanine. Molecular cloning and sequencing of cDNAs encoding the tarantula hemocyanin subunits a and e.";
J. Biol. Chem. 265:19447-19452 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burypelma californica (American tarantula).
Bukaryota, Metazoa, Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Aphonopelma.
NCBI_TaxID=29932;
COPPER 2 (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. ...) (POTENTIAL)

EC2FREDO4935DFBD CRC64;
                                                                                                                                                                                                                      .
0
                                                                                                                                                            Length 628;
                                                                                                                                                         Score 38; DB 1; Length 628
Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hemocyanin A chain (HCA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   630 A.A.
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InterPro; IPR005203; hemocyanin_C.
InterPro; IPR005204; hemocyanin_N.
InterPro; IPR005227; Tyrosinase.
Pfam; PF00372; hemocyanin, 1.
Pfam; PF03723; hemocyanin, C; 1.
Pfam; PF03722; hemocyanin, C; 1.
Pfam; PF03722; hemocyanin, N; 1.
PRINTS; PR00187; HAEMOCYANIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
      365 COJ
450 N-1
617 N-1
72435 MW; J
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                                                                                                                                                         h 62.3%;
Similarity 71.4%;
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                         нимнину 179
      365
450
617
628 AA;
                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                3 HKWHWVV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCYA EURCA
                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                            173
                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
HCYA_EURCA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=95350630, PubMed=7542800,

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

McKenney K., Shirley R., Liu L.I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Grehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D., Peterson J. Hickey E., Dodson R., Gwinn M., Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                       COPPER 1 (PROBABLE).
COPPER 1 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
SOPPER 2 (PROBABLE).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
NCBL_TaxID=727;
                                                        transport; Copper; Glycoprotein; Hemolymph
                                                                                                                                                                                                                                                                                                                                                     Length 630;
                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length 630
Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                              4F6989963C1CC793 CRC64;
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(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
HEMOCYANIN 1; 1.
HEMOCYANIN 2; 1.
TYROSINASE 2; 1.
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174
178
178
205
205
205
325
325
335
345
86
450
N
72187 MW,
                                                                                                                                                                                                                                                                                                                                                   62.3%;
71.4%;
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Query Match
Best Local Similarity 71.4°,
Best Si Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 HHWHWHV 179
                  PROSITE; PS00210; H
PROSITE; PS00498; T
Transport; Oxygen t
INIT MET 174
METAL 178
                                                                                                                                                                                                                                                                                          620
630 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
TWB27 HABIN
AC 086234
DT 30-MAY-2000
DT 30-MAY-2000
DT 30-MAY-2000
DT 28-FEB-2003
DE HYPOTHETICAL
GN HILLST
CC BACTERIA, PY
CC PASTERIALS
CC CASTRAIN-Rd /
RN HILLST
CC STRAIN-Rd /
RN KELIAVAGE FRO
RC STRAIN-Rd /
RN KELIAVAGE AN
RA WEIGHARN A.
RA WEIGHARN T.D., F
RA WEIGHARN T.D., F
RA WEIGHARN T.D., F
RA WHOLE-GEROW
RT RG ";
RA WHOLE-GEROW
RT RG ";
RA ULTERDACT T.C.;
RA WHOLE-GEROW
RT RG ";
RA ULTERDACT T.C.;
RA WHOLE-GEROW
RT RG ";
RA ULTERDACT T.C.;
RA WHOLE-GEROW
RT RG ";
CC THIS SWISS-F
CC CHO ELLOPEAN
CC COT SEND AN
TIGR; HII127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000
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28-FEB-2003
                                                                                                                                                                                           METAL
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                          CARBOHYD
    PROSITE;
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METAL
METAL
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Gaps
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                                                           Score 37; DB 1; Length 138;
Pred. No. 38;
1; Mismatches 0; Indels
  Transmembrane; Complete proteome.
                                         8833E1195A6184EC CRC64;
                                                                                                                                                               December 16, 2003, 14:15:15
                     POTENTIAL.
                                POTENTIAL.
                                131 P
15598 MW;
                                                               60.7%;
                                                                         83.3%;
                                                                         Local Similarity 83.3
Hypothetical protein;
TRANSMEM 12 32
                  62
111
138 AA;
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109 HKFHWV 114
                                                                                                                                                               Search completed: Decemb
Job time: 6.66667 secs
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                                          SEQUENCE
                      TRANSMEM
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anopheles g armigeres s holotrichia

095143 09W1V6 076951 076951 09V551 09V5752 09V573 0907W1 0907047 0907W2 0816K2 0816K2 0916K2 0916K2 0916K2 091743 0907W2 0907W3 0907W3

tenebrio mo

anopheles g aedes aegyp bombyx mori

holotrichia manduca sex aedes aegyp anopheles g anopheles g anopheles s anopheles g

bombyx mori

sarcophaga

anopheles g

Q9gva6 Q25519 Q8mzm4 Q76208

hyphantria

09gvas pimpla hypo

pimpla hypo manduca sex

anopheles g anopheles g aedes aegyp

drosophila drosophila

galleria me

drosophila

OM protein

Run on:

Sequence:

Searched:

Database

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAILMATCC 19089 / CB15;
MEDLINE-21173698; PubMed=11259647;
MIDELINE-21173698; PubMed=11259647;
MIDELINE-21173698; PubMed=11259647;
MIDELINE-21173698; PubMed=11259647;
MIDELINE-21173698; PubMed=11259647;
MIDELINE-21173698; PubMed=11259647;
MIDELINE-21173698; PubMed=11259647;
MIDELINE N.C., Newton A., Stephens C., Phadke N.D., Bly B., Colonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
MCOmplete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. USA. 98:4136-4441(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caulobacter crescentus.
Bacteria, Forebacteria, Alphaproteobacteria, Caulobacterales, Cayrobacteracese, Cayrobacter.
Cayrobacteracese, Caulobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T protein; Complete proteome.
209 AA; 22817 MW; B8C635B8A2643259 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBErel. 17, Created)
01-JUN-2001 (TrEMBErel. 17, Last sequence update)
01-MAR-2002 (FrEMBErel. 20, Last annotation update)
Hypothetical protein CC3059.
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0
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Pred. No. 12;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 AA
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                                                                                                Q9GYW1
097047
096751
09816K2
0816K1
044249
08MZM2
096W2
09GW2
09GW2
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044251
096453
096753
09GVA6
Q25519
Q8MZM4
          Q95R43
Q9W1V6
Q964D5
                                                076951
0811F6
096752
09V521
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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5; Conservative 2
 PRELIMINARY
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Best Local Similarity
Matches 5; Conserv
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CC3059; -.
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Q9A3Z1
SOUR READER READ
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OBP73 xanthomonas
OBP73 xanthomonas
OBP73 xinnia eleg
OBYMS9 rhizobium 1
Q8rMS9 rhizobium 1
Q8rMS4 shewanella
Q8cxg1 pyrobaculum
Q8mp4 caenorhabdi
OBxmg3 epichloe ty
Q8xmg3 epichloe ty
Q8xmg3 exanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8p338 xanthomonas
Q8peh7 xanthomonas
Q92wul rhizobium m
Q9bld9 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9a3z1 caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                  December 16, 2003, 14:09:45; Search time 25 Seconds (without alignments) 92.899 Million cell updates/sec
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                                                                                                                                                                                                                                                       830525
         GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                            - protein search, using sw model
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08P1F4
08P739
09PF80
09PF80
08VM89
08R814
08R814
08R814
08R814
08P84
08P33
08KMG3
09XMG3
09XMG3
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Gapop 10.0 , Gapext 0.5
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sp mammal: *
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sp_virus:*
sp_vertebrate:*
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Maximum DB seq length: 2000000000
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Match
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Perfect score:
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Gaps

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Result è.

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Nature 406:151-159(2000).
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셤
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Auaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertollini M.C., Camargo L.E.A.,

RA Alves L.M.C., do Amaral P.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Formighieri B.F., Faranco M.C., Ferro M.I.T.,

RA Formighieri B.F., Franco M.C., Greggio C.C., Ferro M.I.T.,

Ratiu J.B.C., Machado M.A., Madeira A.M.B.N., Marinera R.G., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

A Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,

A Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Steubal J.C., Kitajima J.P.;

R. "Comparison of the genomes of two Xanthomonas pathogens with differing and the seconds of the seconds of two Xanthomonas pathogens with differing and the seconds of two santos metalogus with differing and the seconds of two santos metalogus with differing and the seconds of two santos pathogens with differing and the seconds of two santos metalogus with differing and the seconds of two santos metalogus with differing and the seconds of two santos metalogus with differing and the seconds of two santos metalogus with differing and the seconds of two santos metalogus with differing and the seconds of the seconds of two santos metalogus with differing and the seconds of two santos metalogus with differing and the seconds of two santos metalogus with differing and the seconds of the seconds of two santos metalogus with differing and the seconds of the seconds of two santos metalogus with differing and the seconds of the seconds of the seconds of the seconds of two santos metalogus with differing the seconds of the se
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STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
Malve A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Berrollini M.C., Camargo L.E.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonas campestris (pv. campestris).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                        Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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213 AA; 23920 MW; 900172C92CE7B10C CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mypothetical protein XCC2775.
                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein XAC2944.
                                                                                                                213 AA
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InterPro; IPR005797; Cytb_b6_N.
PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217;
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                                                                                                            PRELIMINARY;
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Matches 5; Conserv
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Q8P739;
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Q8PIF4;
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                                    RESULT 2
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Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
Ratsuyama A.M., Kishi L.T., Leite R.P., Itemos E.G.M., Lemos M.V.F.,
Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
A Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
A Martine E.C., Maidanis J., Menck C.F.M., Miyaki C.Y. Moon D.H.,
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
A Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
Comparison of the genomes of two Xanthomonas pathogens with differing
That specificities "."
BMEL, AE012390, AAM42047.1; --
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Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L.M.C., Array J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.
A Barros M.H., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Columbo L.L., Cristofani M. Dias FReto B., Docena C., El-Dorry H.,
Raganier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
Racincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Racincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Racincani A.P., Ferreira M.J., Naqueira M.H., Kemper E.L., Kitajima J.P.,
R. Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
R. Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.
R. Hemos B.G.M., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
Macques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Macques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Mani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
R. Honian M.Jr., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
R. Goldwan V.E., Jr., Pesquero J.B.,
R. Ad Silva A.M., da Silva M.M., da Silva W.A., Try Pesquero J.B.,
A da Silva A.C.R., da Silva R.M., da Silva W.A., Trais S.M., Tsuhako M.H.,
R. Ade Souza A.P., Terenzi M.F., Triffi D., Tsai S.M., Tsuhako M.H.,
R. The genome sequence of the plant pathogen Xylella fastidiosa.",
Mathian M. Mathala M. Mathian M. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Xanthomonadaceae; Xylella.
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Pred. No. 12;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome.
SEQUENCE 214 AA; 23740 MW; 0F7BFDCC76937150 CRC64;
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Last annotation update)
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InterPro; IPR005797; Cytb_b6_N.
PROSITE; PS00192; CYTOCHROME_B HEME; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last seq
01-WAR-2002 (TrEMBLrel. 20, Last ann
Hypothetical protein Xf0597.
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71.4%;
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Matches 5; Conservative
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01-JUN-2002 (TrEMBLrel. 21,
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Matches 7; Conservative
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Q8E8L4
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MEDIJNE=20098724; PubMed=10631260;
Percez-Amador M.A., Abler M.L., De Rocher E.J., Thompson D.M.,
Percez-Amador M.A., Abler M.L., Ders A., Green P.J.;
"Identification of BFN1, a bifunctional nuclease induced during leaf
and stem senescence in arabidopsis.";
Plant Physiol. 122:169-179(2000).

FRMB1, U90266; AAD00695.1; -.
HSSP; P24289; LAKO.
                                                                                                                                                                                        Gaps
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"Identification and characterisation of a novel monocarboxylic acid transporter of Rhizobium leguminosarum "; submitted (DEC-2001) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                        0;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.4%; Score 46; DB 10; Length 328; 71.4%; Pred. No. 18; 0; Indels ive 2; Mismatches 0; Indels
                                                                                                                     75.4%; Score 46; DB 16; Length 218; 71.4%; Pred. No. 12; tive 2; Mismatches 0; Indels
EMBL; AE003905; AAF83407.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 218 AA; 24198 MW; A032E2AD602C24B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 AA; 37560 MW; 9343388936C53F7E CRC64;
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Last sequence update)
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Last annotation update)
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Interpro; IPR003154; S1/PInuclease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02265; Nuclease; 1.
PROSITE; PS00190; CYTOCHROME C; 1.
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                                                                                                                                                        Best Local Similarity 71.4
Matches 5; Conservative
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NCBI_TaxID=34245;
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28 LHQWHWI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FLHKWHW 7
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STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
Heidelberg Jf., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
Meyer T., Tsapin A., Scott J., Beanan M., Brinkac D., Daugherty S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Malunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.; Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586."; U. Bacteriol. 184:2005-2018(2002).

EMBL, AR01511; AAL94167.1;
                                                                                                                                                                                                                                                                  Gaps
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Alteromonadaceae, Shewanella.
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                                                                                                                                                                                                  2; Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                  Indels
EMBL; AJ421944; CAD19126.1; -.
InterPro; IPR003594; ATPbind_ATPase.
Pffam; PF02518; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
SEQUENCE 417 AA; 45820 NW; 2034030279B9E996 CRC64;
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SEQUENCE 196 AA; 23169 MW; 4438206B0BCCB0C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical protein FN2083.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved hypothetical protein.
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                                                                                                                                                                                                  75.4%; Score 46; DB 87.5%; Pred. No. 23;
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MEDLINE=21886394; PubMed=11889109;
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"Genome sequence of the nematode C.elegans: A platform for
                               Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                        SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                      67.2%;
50.0%;
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Best Local Similarity 71...,
Aca 5; Conservative
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Best Local Similarity 50...
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94 FMHRFHWI 101
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         SEQUENCE FROM N.A.
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Mitochondrion.
                      Wallis J.M.;
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Q8KQT4
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Rhabditidae, Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
[1]
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Wafadman J., Impraim M., Lee K., Berry K., Lee C., Feldblyun T., Khouri H., Gill J., Utterback T.R., McDonald L.A., Peldblyun T.V., Smith H.G., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium Nat. Biotechnol. 201118181123 (2002).

BMB., AEO15965, AANS7609.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
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                                                                                                                                                                   68.9%; Score 42; DB 16; Length 486; 62.5%; Pred. No. 1.1e+02; tive 3; Mismatches 0; Indels
                                                                                                                   TIGR; SO4649; -.
Hypothetical protein; Complete proteome.
SEQUENCE 486 AA; 57471 MW; B25617A4A982564F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Crenarchaecta; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Last annotation update)
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EMBL; AE009814; AAL63387.1; -.
InterPro; IPR00495; SBP_bac_5.
Pfam; PR00496; SBP_bac_5; 3.
Complete proteome.
SEQUENCE 737 AA; 82378 MW; BCFC9D3E46354725
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                   Dipeptide binding protein. PAE1300.
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Best Local Similarity 62..
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Best Local Similarity 62.5
Matches 5; Conservative
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Y46G5A.33.
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Q8MPP4
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MDDLINE=92145777; PubMed=1782678;
MOGEN K.L., Siegel M.R., Schardl C.L.;
Mogen K.L., Siegel M.R., Schardl C.L.;
"Linear DNA plasmids of the perennial ryegrass choke pathogen Epichloe typhina (Clavicipitaceae).";
Curr. Genet. 20:519-526(1991).
EMBL; X57200; CAA40486.2;
InterPro; IPRO00477; RVTse.
Fran; PRO0078; rvt; 1.
ENA-directed DNA polymerase; Transferase; Mitochondrion; Plasmid.
                                                                                                                                                                              Gaps
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Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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Hypocreales; Clavicipitaceae; Epichloe.
NCBI_TaxID=5113;
                                                                                                                           Score 41, DB 5, Length 145;
Pred. No. 47;
4; Mismatches 0; Indels
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investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL110485; CAD36500.1; -
SEQUENCE 145 AA, 16489 MW; 50B4B1F300F7D357 CRC64;
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Last sequence update)
Last annotation update)
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376 FLHNWGWAI 384
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE 574 AA;
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                                                                              RESULT 14
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SEQUENCE FROM N.A.

SEQUENCE TO N.A.

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RADINE=22022145; PubMed=12024217;

A Barian S.B. Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Alves L.M.C., do Amaral A.M., Berrolini M.C., Camargo L.B.A.,

A Camarotte G., Cannavan F., Cardzoo J.R., El-Dorry H.,

Ratia J.B., Ferrala A.B., Ferrala R.C., Faran M.I.T.,

Ratia J.B., Ferrala A.J.S., Ferrala R.C., Grapton M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Rorali B.C., Machado M.A., Madeira A.M. B.N., Martinez Rossi N.M.,

Martins B.C., Machado M.A., Madeira A.M. B.N., Martinez Rossi N.M.,

Roreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Perindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Spinola L.A.F., Takita M.A., Truffi D., Tsai S.M., White F.F.,

Schubal J.C., Kitajima J.P.;

R. "Comparison of the genomes of two Xanthomonas pathogens with differing the state of the 
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                                                                                                     SEQUENCE FROM N.A.

WEDLINE=22034956; PubMed=12039751;

WEDLINE=22034966; PubMed=12039751;

Yen M.R., Lin N.T., Hung C.H., Choy K.T., Weng S.F., Tseng Y.H.;

"oriC Region and Replication Termination Site, dif, of the Xanthomonas
campestris pv. campestris 17 Chromosome.";

Appl. Environ. Microbiol. 68:2924-2933(2002).

EMBL; AY057934; AAL30086.1; --

EMBL; AX057934; AAL30086.1; --

EMBL; PF02096; 60KD IMP; 1-

PERINTS; PRO0701; 60KDINNERMP.
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Xanthomonadaceae, Xanthomonas.
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Pred. No. 1.8e+02;
1; Mismatches 3; Indels
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Nature 417:459-463 (2002).
EMBL, AB012552; AAW43456.1; -.
InterPro; IPR001708; 60kDa innermeb.
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Xanthomonadaceae; Xanthomonas.
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SEQUENCE FROM N.A.

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SEQUENTIALISES/202145; PubMed-12024217;

MEDINTES-202145; PubMed-12024217;

A Silva A.C.R.; Ferro J.A., Berrolach F.C.; Farah C.S.; Furlan L.R.;

A Lues L.M.C., do Amaral A.M.; Berrolain M.C.; Camargo L.B.A.;

A Lues L.M.C.; do Amaral A.M.; Berrolain M.C.; Camargo L.B.A.;

A Camarotte G. Cannavan F., Cardozo J., Chambergo F.C.; Capina L.P.;

A Camarotte G. Cannavan F., Cardozo J.C., Ferrola L.P.;

A Ratsuyama A.M.; Kishi L.T., Leite R.P.; Lemos B.G.M.; Lemos M.V.F.;

A Ratsuyama A.M.; Kishi L.T., Leite R.P.; Lemos B.G.M.; Lemos M.V.F.;

A Ratsuyama A.M.; Kishi L.T., Leite R.P.; Martinez-Rossi N.M.;

A Martins E.C.; Meidanis J.; Menck C.F.M.; Miyaki C.Y.; Moon D.H.;

A Moreira L.M.; Rovo M.T.M.; Okura V.K.; Oliveira M.C.; Oliveira W.C.;

A Pereira H.A.; Rossi A., Sena J.A.D.; Silva C.; de Souza R.F.;

Spinola L.A.F.; Takita M.A.; Tamura R.E.; Teixeira E.C.; Tezza R.I.D.;

Spinola L.A.F.; Takita M.A.; Tamura R.E.; Teixeira E.C.; Tezza R.I.D.;

A Trindade dos Santos M.; Tutffi D.; Tsai S.M.; White F.F.;

Comparison of the genomes of two Xanthomonas pathogens with differing Nature 417,459-463(2002).
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MEDLINE=21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
                                                                                                                                                                                                                                                                       Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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55.6%; Pred. No. 1.8e+02;
iive 1; Mismatches 3; Indels
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Rhizobiaceae; Sinorhizobium.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RB0238.
RB0238 OR SMB20248.
Rhizobjum meliloti (Sinorhizobium meliloti).
                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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PRINTS; PR00701; 60KDINNERMP.
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Golding B., Puehler A.;
"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S. 98:9889-9894(2001).
EMBL, Al603642; CAC46638.1; -.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 582 AA; 63374 MW; 2E20D8D00DB09B2B CRC64;
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 AAU74684 standard; Peptide;
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20-DEC-2000; 2000US-257007P.
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                                                                                      December 16, 2003, 14:06:05; Search time 33 Seconds (without alignments) 43.289 Million cell updates/sec
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| SIDSI, gcgdata/geneseqp-embl/AA1980.DAT:*
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                                                                                                                                                                                                                                                                1107863
             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                      1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU74683
AAU31978
ABB57797
AAU14133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB59504
ABB57998
AAR89115
AAW14441
                                                                sw model
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                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                               protein search, using
                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
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1755555533
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64
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                                                                                                                                                                     1 FLHKWHWYV 9
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Match 1
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Score

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               whose sequence is based in part on residues 42-50 of human cancer antigen ATF4/CREB-2 (not defined) and the polynucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising and immune ference and at the expense of an antised in vitro or in vivo in the presence and at the expense of an antigen presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune effector cell. The compounds are useful for modulating an immune response to the synthetic and naturally occurring compounds. The compounds are useful for treating cancer, particularly ovacines. The compounds are useful for treating cancer, particularly covarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These antibodies are further useful for immunotherapy when administered to a subject. The peptides, polypeptides and polynucleotides are useful in diagnostic methods, for the detection and purification of antibodies, cor as immunogents a human cancer antigen ATF4/CMFR-2 has antipodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer antigen; ATF4; CREB-2; vaccine; cytostatic; immunogenic ligand; gene therapy; MHC; major histocompatibility complex; adoptive immunotherapy; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                        or as immunogens for the production of antibodies. The present
sequence represents a human cancer antigen ATF4/CREB-2 based immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                  respectively
New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: Immunogenic ligands AAU74681-AAU74686 are stated to be encoded by the degenerate DNA sequences AAS20120-AAS20125 respective) but have not been cross-referenced or CDS features put in due to the degeneracy of the DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                     The invention relates to compounds comprising an immunogenic ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cancer antigen ATF4/CRBB-2 based immunogenic ligand #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 64; DB 23; Length 9; ilarity 100.0%; Pred. No. 9.3e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU74683 standard; Peptide; 9 AA.
                                                           Claim 4; Page 56; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-2000; 2000US-209388P.
20-DEC-2000; 2000US-257007P.
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                                                                                                                                                                                                                                                                                                                                                                                                                      ligand of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FLHKWHWYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENZ ) GENZYME CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FLHKWHWYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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The invention relates to compounds comprising an immunogenic ligand whose sequence is based in part on residues 42-50 of human cancer antigen ATF4(TRBE-2 (not defined) and the polyvucleotides encoding them. Also included are an antibody that specifically recognises and binds the compound, a method for inducing an immune response in a subject by delivering the compound, a method of immunotherapy comprising the compound, a method of immunotherapy comprising the compound and the presence and at the expense of an attigen presenting cell that presents the immunogenic compound in the context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response context of an MHC (major histocompatibility complex) molecule and a method of adoptive immunotherapy comprising administering the immune response to the synthetic and naturally occurring compounds. The compounds are useful for modulating an immune response covarian cancer. The compounds are useful for treating cancer, particularly covarian cancer. The compounds are also useful for generating antibodies that specifically recognise and bind to these molecules. These compounds continued to the semilation of antibodies are useful in diagnostic methods, for the detection and purification of antibodies. The sequence represents a human cancer antigen ATF4(CRB-2 based immunogenic invarian the present
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                                                                                                                                       New therapeutic compounds comprising immunogenic ligands, useful for modulating an immune response, particularly for treating ovarian cancer, and as components of anticancer vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU31978 standard; Protein; 556 AA
                                                                                                                                                                                                                                                                                                                         English.
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26-JAN-2001; 2001US-0770160.
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ligand of the invention.
                                                                                                                                                                                                                                                                                                                         Claim 3; Page 55; 68pp;
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                                                                       WPI; 2002-097764/13.
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Nicolette CA;
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New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                             Claim 20; Page 534; 765pp; English.
                                                                                                                                                                                                                                                                           ABB57797 standard; Protein; 512 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                PWD,
                Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ξ
                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
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                                                                                                                                                                                                                                           74 FLHSWWWY 81
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N-PSDB; ABL01900.
                              WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY.
                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                          556 AA;
                                                                                                                                                                                                                               1 FLHKWHWY
      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                           WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                   pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001.
                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                        ABB57797;
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                  Matches
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01640-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunomodulatory, cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiaethmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
                                                                      Disclosure; SEQ ID NO 183; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              68.8%; Score 44; DB 22;
83.3%; Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                   512 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-451939,
N-PSDB; AAS22438
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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ID AATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
    à
                                                                                                                                                                                                                                                                                           LINCALIDED ACALGES TO MOVEL HUMBAN SCLEECE POLYPEPTIGES. THE POLYPEPTIGES and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physological interactions of the polypeptide. Vectors comprising the mucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and cells proteins. They and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or nerve tissue growth or regeneration; in treatment of leukaemias. AAU25510-AAU33304 represent the amino acid in sequences of novel human secreted proteins of the invention.
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                                                                                                                                                               Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                 invention relates to novel human secreted polypeptides. The
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The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as

Example 4; Page 522-523; 894pp; English.

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Gaps

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insecticides, therapeutics and pharmaceutical drugs. The invention

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molecular weight markers, food supplements, and in antibody production.

The polypeptides are used to identify compounds which bind to the polypeptides. Polymucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or production of recombinant proteins, and in generating anti-sense DNA or target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Colypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, cligament and/or nerve tissue, wound healing, treating burns, promoting contraceptive, treating osteoporosis and osteoarthritis, anemaia, contraceptive, treating osteoporosis and osteoarthritis, anemaia, alleration or from autoinmunity, cancer, alleray, asthma, clungal infection or from attoinmunity, cancer, alleray, asthma, cantillammatory diseases, nervous system disorders, and infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 5304; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 554;
                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 5304.
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 22;
Pred. No. 1.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB59504 standard; Protein; 683 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                           68.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
N-PSDB; ABL03607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 HPWHWY 311
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                                                                                                                                                                                                                                                                                                                                                                                           554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 HKWHWY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB59504;
                                                                                                                                                                                                                                                                                                                                                                                              Seguence
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                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01875) and the encoded proteins
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                                                                                                                                                                                Gaps
         discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila, developmental biology; cell signalling; insecticide; pharmaceutical.
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                                                                                                                                                Length 683;
                                                                                                                                  Score 44; DB 22; Length booperd. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 786.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers EW;
                                                                                                                                                                                                                                                                                                                       ABB57998 standard; Protein; 684 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PWD,
                                                                                                                                               68.8%;
62.5%;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                5; Conservative
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                                                                                                                                                                                                             2 LHKWHWYV 9
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                                                                                                                                                Query Match
Best Local Similarity
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
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                                                                                                                       683 AA;
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                                                                                                                       Sequence
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This protein is a prophenol oxidase derived from a domestic silkworm. The phenol oxidase may be used as a novel labelling oxidase. The cludidation of the primary structure of the prophenol oxidase will contribute to the reconstitution of a prophenol oxidase activation system which can be applied to the detection of microorganisms by measurement of beta-1,3-glucan and peptide glycan.
            oxidase; prophenol; phenol; domestic silkworm; label; detection
                                                                                                                                                                                                                                                                                                                                                              (Pro)phenol oxidase derived from a domestic silkworm - useful labelling oxidase and in pro-phenol oxidase activation system detection of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 62.5%; Score 44; DB 18; Length 685; Similarity 62.5%; Pred. No. 1.6e+02; 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus cellular proliferation protein #333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense, prokaryotic cellular proliferation protein, antibiotic, antibacterial, drug design.
                                                                                 1..52
/label= pro-sequence
53..685
/label= phenol_oxidase
/note= "claim I"
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 14-17; 18pp; Japanese.
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU34057 standard; Protein; 142 AA.
                                                                                                                                                                                                                                                                                       (WAKP ) WAKO PURE CHEM IND LID
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
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N-PSDB; AAT62660.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     685 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200170955-A2.
                                                                                                                                                                       JP09023886-A.
                                                                                                                                                                                                                                 13-JUL-1995;
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                                          Bombyx mori.
                                                                                                                                                                                                    28-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                       Key
Peptide
                                                                                                                 Protein
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AAU34057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Pro) phenol:oxidase from silkworm - useful as a labelling oxidase
                                                                                                                                                                                                                              Silkworm; larvae; pro; phenoloxidase; Phe52-Val693; Phe52-Gly685 labelling oxidase.
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                                                                                                                                                                                                    Bombyx mori (pro)phenoloxidase Phe52-Gly685.
                                                                                                                                                                                                                                                                                                                                                                            41..51
/note= "peptide fragment"
                                                                                                                                                                                                                                                                                                                                                             "peptide fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                    "peptide fragment"
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                                                                                                                                                                                                                                                                                                     cocation/Qualifiers
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                                                                                                                 AAR89115 standard; Protein; 685 AA.
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/note= '
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                                        206 LHHWHWHL 213
               LHKWHWYV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       685 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP07289251-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1994;
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                                                                                                                                                                                                                                                                           Bombyx mori
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                                                                                                                                            AAR89115;
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AAN1441
ID AAW1
XX
AC AAW1
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DT 15-M
XX
                                                                                    RESULT 8
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27-NOV-2000;
22-DEC-2000;
                                                                                          famamoto RT,
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 23-OCT-2000;
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08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
ABP39358
à
                                                                                                                                                                                                  The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are secherichia coli, Staphylococcus almonella typhi, Klebsiella pneumoniae, Pseudomonnas aeruginosa and Bnterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen of for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Con the printed specification, but was obtained in electronic form part directly from MIPO at
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                                                                           Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                 New polynucleotides for the identification and development of
antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.2%; Score 43; DB 22; Length 142; 75.0%; Pred. No. 50; 1; Indels 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus cellular proliferation protein #946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                    Example 3; Seq ID No 5553; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU36776 standard; Protein; 147 AA.
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001; 2001WO-US09180.
         27-NOV-2000; 2000US-253625F.
22-DEC-2000; 2000US-257931F.
16-FEB-2001; 2001US-269308F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                         (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus
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21 LHNFHWYV 28
                                                                                                                 WPI; 2001-611495/70.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              142 AA;
                                                                                                                             N-PSDB; AAS51916
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                                                                               Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2002
 23-OCT-2000;
27-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential genes their between the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC genemoniae, Pseudomonas aeruginosa and Enterococcus facefalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to invention antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The protein compounds in required for cell proliferation in can wide variety of organisms. The protein sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epidermidis; open reading frame; ORF; bacterial infection;
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                                                                                                                                                                                                                         Carr GJ;
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                                                                                                                                                                                                                      Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 22; Length 147; pred. No. 52; 1; Mismatches 1; Indels
                                                                                                                                                                                                                      Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Seq ID No 12369; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP39358 standard; Protein; 166 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-055779P
97US-064964P
2000US-242578P.
                       2000US-253625P.
                                                                                        16-FEB-2001; 2001US-269308P.
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                                                                                                                                                                                                                      Ohlsen KL,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                            (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || :||||
25 LHNFHWYV 32
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Best Local Similarity
Matches 6; Conserv
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenee), comparising one of 5481 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromosome processes and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                            DB 23; Length 235;
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                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 82;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            67.2%; Score 43; 40.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #19697.
              Claim 1; Page 3373; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG19706 standard; Protein; 1248 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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82 FMHRWATKKGLHWYL 96
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                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                           Streptococcus proteins
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                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                            235 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS83893
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial, antinflammatory; infection, vaccine, meningitis, gene therapy.
                                                                                                                                                                                              ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                              67.2%; Score 43; DB 23; Length 166; 75.0%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus polypeptide SEQ ID NO 2222.
                                                                                                                                                                  Disclosure; SEQ ID 4203; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP26523 standard; Protein; 235 AA.
(GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-2001; 2001WO-GB04789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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                                                                  WPI; 2002-381255/41.
N-PSDB; ABN91903.
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Best Local Similarity
                                 Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                              166 AA;
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                                                                                                                                                                                                                                                                                                                                                                             USPTO web site.
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Gaps

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conditions and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags confidentifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving confidence of (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating clasorates involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in claspostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1248 AA;
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0;
                               Gaps
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0
67.2%; Score 43; DB 22; Length 1248; 83.3%; Pred. No. 4e+02; 1; Mismatches 0; Indels
                               5; Conservative
              Best Local Similarity
  Query Match
                               Matches
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LHOWHW 1070 2 LHKWHW 7 1065 ð Db

RESULT 15 ABJ10988 ABJ10988;

ABJ10988 standard; Protein; 98 AA.

(first entry) 10-DEC-2002 Yeast selected interacting domain protein SEQ ID NO: 110.

Yeast, protein-protein interaction, Selected Interacting Domain, SID (RTM); secretion yield; cancer; neurodegenerative disease; fungicide; cytostatic; neuroprotective. 

Saccharomyces cerevisiae.

WO200266504-A2.

29-AUG-2002.

14-FEB-2002; 2002WO-EP02299.

16-FEB-2001; 2001US-269266P

(HYBR-) HYBRIGENICS

Legrain P;

WPI; 2002-674913/72. N-PSDB; ABT11305.

drug screening or development, for developing yeast strains with better secretion yield of protein, or in gene therapy (e.g. to treat Candida infection or cancer) New protein-protein complexes of Saccharomyces cerevisiae, useful in

Claim 6; Page 71; 357pp; English.

The present invention relates to complexes between Saccharomyces cerevisiae Selected Interacting Domain (SID (RTM)) proteins and coding sequences. The protein complexes of S. cerevisiae are useful in drug development, in screening drugs or agents that modulate the interaction of proteins, for developing yeast strains with better secretion yield of

protein, and in gene therapy. The protein complexes, polypeptides and polymucleotides are useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in humans or animals. The present sequence is a protein of the invention. 88888

98 AA; Sequence

Gaps . 0 Similarity 100.0%; Score 42; DB 23; Length 98; Similarity 100.0%; Pred. No. 49; 5; Conservative 0; Mismatches 0; Indels Local Similarity Query Match Best Loc Matches

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74 KWHWY 78 4 KWHWY 8 ð 셤

Search completed: December 16, 2003, 14:14:29 Job time : 34 secs

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Sequence 5382, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                          Appli
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                                                                                                                                                               Sequence
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ADDRESSES: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                          PCT-US94-01553A-32
PCT-US94-01553A-36
PCT-US95-10426-32
PCT-US95-10426-36
                                                     US-09-537-168-4
US-09-577-168-6
US-09-672-459-2
US-09-636-252A-13
US-09-31-687-6
US-09-381-687-8
US-09-545-586-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                    US-08-468-220-37
US-08-468-698-37
US-08-194-664A-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 191 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5382:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
CQUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
OMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
 RESULT 1
US-09-107-532A-5382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
 Sequence 5382, Ap
Sequence 4203, Ap
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 34, Appli
Sequence 34, Appli
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                                                                                                2003, 14:11:00 ; Search time 12.3333 Seconds (without alignments) 30.875 Million cell updates/sec
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Sequence 34
Sequence 13
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Sequence 3
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US-09-183-412-5

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US-08-468-698-36

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Listing first 45 summaries
                                                                    protein search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. 67;
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100.0%; Pred. No. c.
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APPLICANT: Svendeen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen Henrik
TILE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276.200-US
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-3
EARLIER FILING DATE: 1997-10-38
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APPLICANT: Syrulff, S ren
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: -Amylase Variants
FILE REFERENCE: 5709.000-US
CURRENT APPLICATION NUMBER: US/09/193,068
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                        RESULT 4
US-09-170-670-5
; Sequence 5, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
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; ORGANISM: B. amyloliquefaciens
US-09-170-670-5
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; ORGANISM: B. amyloliquefaciens
US-09-193-068-5
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Best Local Similarity 100.
Matches 5; Conservative
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                                                 152 KWHWY 156
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4 KWHWY 8
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LENGTH: 480
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Sequence 4203, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS

TITLE OF INVENTION UNMER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4203

LENGTH: 166
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                   Query Match 70.3%; Score 45; DB 4; Length 191; Best Local Similarity 75.0%; Pred. No. 12; Matches 6; Conservative 2; Mismatches 0; Indels
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Pred. No. 20;
1; Mismatches 1; Indels
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APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Torben
APPLICANT: Borchert, Torben
APPLICANT: Baggard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796,204-08
CURRENT APPLICATION NUMBER: 055/96
EARLIER APPLICATION NUMBER: 0515/96
EARLIER PILING DATE: 1996-06-28
EARLIER PILING DATE: 1996-06-28
EARLIER PILING DATE: 1996-06-28
EARLIER PILING DATE: 1996-06-28
EARLIER PILING DATE: 1996-0719
EARLIER PILING DATE: 1996-0719
EARLIER FILING DATE: 1996-0719
EARLIER FILING DATE: 1996-0711
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09182859; Patent No. 6143708; GENERAL INFORMATION:
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Best Local Similarity 75.0
Matches 6; Conservative
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52 LHQYHWYV 59
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Gaps
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APPLICANT: Outtrup, Helle
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, Bjarne Ronfeldt
APPLICANT: Nielsen, black Skvygaard
APPLICANT: Nielsen, vibeke Skvygaard
APPLICANT: Noe'k, Lisbeth Hedegaard
ITLE OF INVENTION: No. 6528296al -Amylase And -Amylase Mutants
ITLE OF INVENTION: No. 6528296al -Amylase And -Amylase Mutants
ITLE OF INVENTION NUMBER: US/09/545,586
CURRENT FILING DATE: 2000-04-07
PRIOR PPLICATION NUMBER: US/09/290,734
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 35
SOOTWARE: FRSESEQ for Windows Version 3.0
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APPLICANT: BOCAGEACT, TAIDEN
APPLICANT: BEGGATG-FYENTEAN, HENTIK
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672,459
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR PILING DATE: 1998-00-29
PRIOR PILING DATE: 1996-06-28
PRIOR PILING DATE: 1996-06-28
PRIOR PILING DATE: 1996-07-11
PRIOR PILING DATE: 1996-10-8
SOFTWARE: PASLESQ for Windows Version 3.0
SSOFTWARE: PASLESQ for Windows Version 3.0
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; ORGANISM: Bacillus amyloliquefaciens
US-09-672-459-4
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Bisgard-Frantzen Henrik
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Patter No. 6528298
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
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Best Local Similarity 100.
Matches 5; Conservative
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US-09-545-586-5
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| Sequence 5, Application US/09290734 |
| Patent No. 6361899 |
| GENERAL INFORMATION: |
| APPLICANT: Svendsen, Allan |
| APPLICANT: Borchert, Torben Vedel |
| APPLICANT: Bisgard-Frantzen Henrik |
| APPLICANT: Outtrup, Helle |
| APPLICANT: Outtrup, Helle |
| APPLICANT: Nielsen, Vibeke Skovgaard |
| APPLICANT: Nielsen, Vibeke Skovgaard |
| APPLICANT: Nielsen, Wibeke Skovgaard |
| APPLICANT: Heeck, Lisbeth Hedegaard |
| TILLE OF INVENTION: No. 6361989el -Amylase Mutants |
| FILE REFERENCE: 5276,400-US |
| CURRENT APPLICATION: NUMBER: US/09/290,734 |
| CURRENT FILING DATE: 1999-04-13 |
| NUMBER OF SEQ ID NOS: 35 |
| SEQ ID NO S |
| LENGTH: 480 |
| LENGTH: 480 |
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                     APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Djarne
APPLICANT: Niesen, Torben L.
APPLICANT: Niesen, Torben L.
APPLICANT: Niesen, Torben L.
APPLICANT: Niesen, Torben L.
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5369.200-020
CURRENT APPLICATION NUMBER: US/09/183,412
CURRENT FILING DATE: 1998-10-30
BARLIER APPLICATION NUMBER: 60/093,234
BARLIER FILING DATE: 1997-11-06
BARLIER FILING DATE: 1997-11-06
BARLIER FILING DATE: 1997-10-30
BARLIER FILING DATE: 1998-10-14
BARLIER FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTSEQ for Windows Version 3.0
SSERICH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bacillus amyloliqufaciens
US-09-183-412-5
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Patent No. 6436888
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-09-290-734-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 KWHWY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 KWHWY 156
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US-09-672-459-4
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Score 42; DB 1; Length 483;
Pred. No. 68;
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                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-468-220-32
is Sequence 32, Application US/08468220
is Sequence 32, Application US/08468220
is Sequence 32, Application US/08468220
is SENERAL INFORMATION:
is APPLICANT: Antrim, Richard L.
is APPLICANT: Mitchinson, Colin
is APPLICANT: Mitchinson, Colin
is APPLICANT: Nower, Scott D.
is APPLICANT: Solheim, Leif P.
if TILE OF INVENTION: Oxidatively Stable Alpha-Amylase
in MUMBER OF SEQUENCES: 68
is CORRESPONDENCE ADDRESS:
is ADDRESSER: Genemoor International, Inc.
is STREET: 180 Kimball Way
is CITY: South San Francisco
                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,220
FILING DATE: 06-UN-95
                                                                                           65.6%; Scor.
100.0%; Pred. No. co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION NUMBER: 08/016,395
FILING DATE: 11-FEB-93
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,696
REFRENCE/DOCKET NUMBER: 35,696
REFRENCE/DOCKET NUMBER: GC220D1
TELECOMMUNICATION INFORMATION:
TELEPRANCE (415) 742-7555
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 amino acids
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Best Local Similarity 100.9
Matches 5; Conservative
                                                                                                               Query Match 65.6
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-220-32
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                      154 KWHWY 158
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                                                                                                                                                                                                                                        4 KWHWY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-468-220-36
                                                    US-08-645-971-2
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| Patent No. 5763385
| GENERAL INFORMATION: Application US/08645971
| TITLE OF INVENTION: Modified Alpha-Amylases Having Altered TITLE OF INVENTION: Calcium Binding Properties NUMBER OF SEQUENCES: 5
| COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER PREADABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER PREADABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER PREADABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER PREADABLE FORM: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/645,971
| INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 483 amino acids TYPE: Application No. 2: APPLICATION DATA: APPLICATION NUMBER US/08/645,971
| TYPE: Amino acids TYPE:
                                                                                                                                                                                                                                                                                                                             CUNTY: SCA.

STATE: CA

CUNTRY: USA

ZIP: 94000

COMPUTER: BEDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,700
FILING DATE: 06-JUN-1995
CLASSIFICATION: 25-2
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: 37,42-7555
TELEPAX: (415) 742-7555
TELEPAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TTELEPAX: anino acids
TTELEPAX: SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.6%; Score 42; DB 1; Length 483; 100.0%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
APPLICANT: CALLON:
APPLICANT: CAROL A. REQUADT
APPLICANT: TRACI H. ROPP
APPLICANT: TERCI H. ROPP
APPLICANT: LEIF P. SOLHBIM
TITLE OF INVENTION: MUTANT ALPHA-AMYLASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Geneman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bb.c.,
100.0%; Preα, ...
                                                                                                                                                                                                                                                                                      ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.6
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 KWHWY 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-08-645-971-2
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Query Match 65.6%; Score 42; DB Best Local Similarity 100.0%; Pred. No. 68; Matches 5; Conservative 0; Mismatches
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Patent No. 5849549
              STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 483 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 KWHWY 158
                                                                       CA
USA
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                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-468-698-32
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                                                                                                                  APPLICANT: Barnett, Christopher
APPLICANT: Barnett, Christopher
APPLICANT: Barnett, Colin
APPLICANT: Requadt, Carol
APPLICANT: Requadt, Carol
APPLICANT: Sequence, Leif P.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/08468698
; Patent No. 5845549
; GENERAL INFORMATION:
APPLICANT: Antrim, Richard L.
APPLICANT: Mitchinson, Colin
APPLICANT: Power, Scott D.
APPLICANT: Solheim, Leif P.
; TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMPLES: CAR
COUNTRY: CAR
ZIP: 94080
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DALENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/468,220
FILING DATE: 06-UN-95
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION NUMBER: 08/194,664
FILING DATE: 11-FEB-93
ATPLICATION NUMBER: 08/106,395
FILING DATE: 11-FEB-93
ATPLICATION NUMBER: 35,696
REFERENCE/COCKET NUMBER: 35,696
REFERENCE/CATION NU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 68;
Mismatches
Sequence 36, Application US/08468220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; P.
Matches 5; Conservative 0;
                                                                                                    APPLICANT: Antrim, Richard L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                   Patent No. 5824532
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 KWHWY 158
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APPLICANT: Antrim, Richard L.

APPLICANT: Barnett, Christopher

APPLICANT: Barnett, Christopher

APPLICANT: Brinett, Colin

APPLICANT: Requadt, Colin

APPLICANT: Rower, Scott D.

APPLICANT: Rower, Carol

APPLICANT: Solheim, Leif P.

TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genencor International, Inc.

STREET: 180 Kimball Way

CITY: South San Francisco

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 483; 68;
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb

COMPUTER IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPOTER: IBM PC COMPATIBLE

APPLICATION NUMBER: U8/08/468,698

FILING DATE: 10-FEB-94

PRIOR APPLICATION NUMBER: 08/016,395

PLING DATE: 11-FEB-94

PRIOR APPLICATION NUMBER: 08/016,395

PLING DATE: 11-FEB-93

ATTORNEY/AGENT INFORMATION:

NAME: STOOM: Christopher L.

REGISTRENCE/DOCKET NUMBER: GC220D2

TELECOMMUNICATION NUMBER: 35,696

REFERENCE/DOCKET NUMBER: 35,696

TELECOMMUNICATION NUMBER: 35,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTAL.

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWAING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,698
FTITING DATE: 06-JUN-95
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Query Match
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/016,395
FILING DATE: 1.FEB-93
ATTORNEY/AGRYI INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 742-7555
TELEFAX: (415) 742-7
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Search completed: December 16, 2003, 14:20:40 Job time : 12.3333 secs ||||| 154 KWHWY 158 4 KWHWY 8 à g

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Gaps 0;

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APPLICANT: Charles A. Nicolette
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REFERENCE: 69126881209900
CURRENT APPLICATION NUMBER: US/09/870,089B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
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Sequence 4, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 30, Appli
Sequence 30, Appli
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Sequence 7, Appli
Sequence 5553, Ap
Sequence 12369, A
Sequence 5, Appli
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Sequence 13, Appl
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                                                                                                                                                                            December 16, 2003, 14:18:11; Search time 22.1667 Seconds (without alignments) 75.512 Million cell updates/sec
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| cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/PCT_MBW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/PCT_MBW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/US06_NBW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/US06_NBW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/US07_NBW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/US08_NBW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/US08_NBW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*
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| cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/US10_NBW_PUB.pep:*
GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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2 US-09-870-089B-7

US-09-815-242-5553

US-09-615-242-12369

US-09-769-864-5

US-09-769-864-4

US-09-769-864-4

US-09-854-346-8

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US-09-918-543-10

US-09-918-543-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    684280 seqs, 185983659 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Gaps

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Indels

6.1e+05;

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Sequence 4, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 114, Appli
Sequence 114, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 22, Appli
Sequence 23, Appli
Sequence 512, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                             Sequence 34285, A
Sequence 204, App
Sequence 33721, A
Sequence 13494, A
                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09970009B
Publication No. US20030175254A1
Publication No. US20030175254A1
APPLICANT: Charles A. Micolette
TITLE OF INVENTION THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
FILE REPRENEUR: 60126081209900
CURRENT APPLICATION NUMBER: US/09/870,089B
                                                                                                                    2 US-09-870-0898-5

5 US-10-125-567A-302

5 US-10-125-567A-302

5 US-10-135-761-7672

5 US-10-136-761-7672

2 US-10-238-075-693

0 US-09-843-676-4

1 US-09-486-4

5 US-10-054-136-4

5 US-10-054-295-4

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5 US-10-054-295-4

6 US-09-864-761-4

7 US-09-864-761-4
is us-10-186-042-2
is us-10-146-327-4
is us-10-146-327-6
is us-10-105-733-8
is us-10-105-733-8
is us-10-199-922-2
is us-10-199-922-2
is us-10-199-922-2
is us-10-184-771-4
is us-10-81-872-114
is us-09-870-069B-3
us-09-732-618-24
us-09-732-618-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 64; DB 12; 100.0%; Pred. No. 6.1e+05;
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US-09-815-242-13494
                                                                                                                                                                                                                                                    US-10-076-604-204
                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 9
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US-09-870-089B-9
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ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                          Query Match 87.5%; Score 56; DB 12; Length 9; Best Local Similarity 88.9%; Pred. No. 6.1e+05; Matches 8; Conservative 0; Mismatches 1; Indels
CURRENT FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 9
                                                                                                                                                                                                                                                                Sequence 5553, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; CRCANISM: Staphylococcus aureus; US-09-815-242-5553
                                                                                               ; OTHER INFORMATION: ATF4/CREB-2
US-09-870-0898-7
                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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21 LHNFHWYV 28
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US-09-815-242-5553
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LENGTH: 142
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Sequence 12369, Application US/09815242; Patent No. US20020061569A1

US-09-815-242-12369

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                APPLICANT: Haselbeck, Kopert
APPLICANT: Haselbeck, Kopert
APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: DEVARYOTES
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-26
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-27
PRIOR PLING DATE: 2001-12-16
PRIOR PLING DATE: 2001-12-16
PRIOR PLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE FASTSEQ for Windows Version 4.0
SEQ ID NO 12369
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APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Carsten
APPLICANT: Andersen, Carsten
APPLICANT: Nissen, Torben L.
APPLICANT: N
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
LENGTH: 480
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; ORGANISM: Bacillus amyloliqufaciens
US-09-769-864-5
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APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 LHNFHWYV 32
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APPLICANT: No. USCO20068352Alozymes A/S
APPLICANT: Svendsen, Allan
APPLICANT: Jorgensen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
FILE REPERENCE: 6140.200-US
CURRENT APPLICATION NUMBER: US/09/854,346
CURRENT PILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 483
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100.0%; Pred. No. 2.7e+02; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Bacillus licheniformis
US-09-854-346-8
       Best Local Similarity 100.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                           APPLICANT: SVENGREL, ALIGH
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
TITLE OF INVENTION: Alpha-Amylase Mutants
TITLE OF INVENTION: Alpha-Amylase Mutants
CURRENT FILING DATE: 2002-06-28
RIOR APPLICATION NUMBER: US/09/672,459
PRIOR PILING DATE: 1998-10-29
PRIOR PILING DATE: 1998-10-29
PRIOR PILING DATE: 1996-04-30
PRIOR PILING DATE: 1996-06-28
PRIOR PILING DATE: 1996-01-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR PILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FRASERG FOR WINGOWS VERBION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Bjarne
APPLICANT: Nissen, Torben I.
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REPERRNCE: 5368.200-05
CURRENT APPLICATION NUMBER: U$/09/769,864
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR PLING DATE: 1998-10-30
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bacillus amyloliquefaciens US-10-186-042-4
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; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
                                                                                                                                                                                                    Sequence 4, Application US/10186042; Publication No. US20030171236A1; GENERAL INFORMATION: APPLICANT: Svendsen, Allan
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LENGTH: 483
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US-09-769-864-4
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Length 483;

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65.6%; Score 42; DB 10; 1
100.0%; Pred. No. 2.7e+02;
iive 0; Mismatches 0;
                                               TYPE: PRT (CRANISM: Bacillus licheniformis US-09-918-543-30
                                                                                                                                  Query Match 65.6 Best Local Similarity 100. Matches 5; Conservative
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US-09-925-576C-8
         ; SEQ ID NO 30
; LENGTH: 483
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LENGTH: 483
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Sequence 10, Application US/09918543

Sequence 10, Application US/09918543

Sequence 10, Application US/002015574A1

Septicant No. US20020155574A10zymes A/S

APPLICANT: Thisted, Thomas

APPLICANT: Andersen, Carsten

APPLICANT: Puglsang, Claus Crone

ITILE REFERENCE: 1006-105 000-05

CURRENT APPLICATION NUMBER: US/09/918,543

CURRENT FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin version 3.1

SEQ ID NO 10
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Fatent No. US20020155574A1
Fatent No. US20020155574A1
FAPLICANT: No. US20020155574A1czymes A/S
APPLICANT: Thisted, Thomas
APPLICANT: Thisted, Thomas
APPLICANT: Figerulf, Soren
APPLICANT: Fuglsang, Claus Crone
TITLE OF INVENTION: Alpha-amylase mutants with altered properties
FILE REFERENCE: 10062.200-US
CURRENT APPLICATION NUMBER: US/09/918,543
CURRENT APPLICATION NUMBER: 2001-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
APPLICANT: No. US20020155574Alozymes A/S
APPLICANT: Thisted, Thomas
APPLICANT: Kjaerulff, Soren
APPLICANT: Andersen, Carsten
APPLICANT: Andersen, Carsten
APPLICANT: Fuglsang, Claus Crone
TITLE OF INVENTION: Alpha-amylase mutants with altered properties
FILE REPERENCE: 10062_200-US
CURRENT APPLICATION NUMBER: US/09/918,543
NUMBER OF SED NOS: 30
SOFTWARE: PatentIn version 3.1
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100.0%; Pred. No. 2.7e+02;
vative 0; Mismatches 0;
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; ORGANISM: Bacillus amyloliquefaciens
US-09-918-543-10
                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Bacillus licheniformis US-09-918-543-8
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US-09-918-543-30
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LENGTH: 483
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Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0;
Sequence 8, Application US/09925576C
Publication No. US20030129718A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Borchert, Torben Vedel
APPLICANT: Nielsen, Bjarne Ronfeldt
TTILB OF INVENTION: Amylase Variants
TTILB OF INVENTION: Amylase Variants
CURRENT APPLICATION UNBER: US/09/925,576C
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Version 3.1
SEQ ID NO 8
LENGTH: 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-925-576C-10

Sequence 10, Application US/09925576C

Publication No. US20030129718A1

GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne Nonfeldt
ITPLIGANT: Nielsen, Bjarne Ronfeldt
ITPLIG OF INVENTION: Amylase Variants
FILE REFERENCE: 10004.204-US

CURRENT APPLICATION NUMBER: US/09/925,576C

CURRENT FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-925-576C-8
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RESULT 15

'Sequence 13, Application US/10184771
'Sequence 13, Application US/10184771
'Sequence 13, Application US/10184771
'Sequence 13, Application US/10184771
'Sequence 13, Application No. US2003017076941
'APPLICANT: Sendsen, Allan
'APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben vedel
'TITLE OF INVENTION: Albha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/10/184,771
'PRIOR APPLICATION NUMBER: US/09/636,252
'PRIOR PILING DATE: 1996-07-18
'NUMBER OF SEQ ID NOS: 16
'SOFTWARE: FastSEQ for Windows Version 3.0
'SOFTWARE: FRT
'ORGANISM: Bascillius
'US-10-184-771-13

Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Copp.
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Search completed: December 16, 2003, 14:41:06 Job time: 22.1667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 16, 2003, 14:10:15; Search time 10.3333 Seconds (without alignments) 83.760 Million cell updates/sec Run on:

US-09-870-089B-9 1 FLHKWHWYV 9 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

		ó			SUMMARIES	
Result No.	Score	Query Match	% Query Match Length	DB	ΩI	Description
1	45	70.3	153	7	G69660	metal-regulated pr
C)	44	68.8	145	7	H69618	stress- and starva
m	44	68.8	-	7	C75311	conserved hypothet
4	44	68.8	4.	N	T51430	dolichyl-phosphate
Ŋ	44	68.8	w	ď	871751	dolichyl-phosphate
Q	43	67.2	147	~	H90007	general stress pro
7	43		209	~	A87628	Φ
æ	43	67.2	218	~	G82786	conserved hypothet
σ	43	67.2	299	ď	PT0060	N-acetylphosphinot
10	43	67.2	299	N	A47031	bialaphos acetylhy
11	43	67.2	w	ч	BHTLA	hemocyanin chain a
12	42	65.6	N	(7	T16945	hypothetical prote
13	42	65.6	un.	Н	ALBSL	alpha-amylase (EC
14	42	65.6	u,	<b>~</b>	ALBSN	alpha-amylase (EC
15	42	65.6	9	Н	BHTLE	hemocyanin chain e
16	42	65.6	9	~	S67964	hemocyanin chain 6
17	41	64.1	193	~	A11904	hypothetical prote
18	41	64.1	CA	~	AG2462	
19	41	64.1	143	7	AF2129	ical
20	41	64.1	4	~	G88979	4.
21	40	62.5	_	7	B83777	stress- and starva
22	40	62.5	-	~	\$28082	vif protein - simi
23	40	62.5		~	G75174	hypothetical prote
24	40	62.5	"	N	H71039	
25	40	62.5	w	Н	BHTLD	Z,
26	40	62.5	62	٦	BHHC2A	hemocyanin subunit
27	33		27	7	T50986	hypothetical prote
28	39	60.9		7	C89961	
29	39		53	~	H87347	

ALG6 protein - yea	TOWN DEPOTE	himothetical prote	transposase [impor	unknown in ISIN [i	bacterioferrin Fl	enterohemolysin 2	hypothetical prote	hypothetical prote	hypothetical prote	spore coat polysac	probable membrane	phosphodiesterase/	probable exported	hypothetical prote
S61985	1,000,0	30114/	E90791	A85652	JS0097	JN0846	T37187	A99775	D85637	E69717	S19439	AC2085	AB0005	T22351
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544	200	110	145	145	177	193	200	257	257	339	512	530	569	634
6.09	. 0	60.0	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4	59.4
33	ח ר ח ר	η c	n 00	38	38	38	38	38	38	38	38	38	38	38
9.5	- C	ų r	J 44	ហ	9	7	00	σ	0	-1	0	۳	4	ហ

## ALIGNMENTS

RESULT 1

099695

metal-regulated protein mrgA - Bacillus subtilis
N;Alternate names: metalloregulation DNA-binding stress protein mrgA
C; Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence revision 05-Dec-1997 #text change 20-Jun-2000
C; Accession: G69660; S70240; B48656; ~D44519; S35938
R; Kunst, F.; Ogasawara, N.; Moszg. I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Bhrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D. Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Kroqh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M., Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A; Authors Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serc
akeuchi M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A; Aychors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

Affile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. Affeterence number: A69580; MUID: 98044033; PMID: 9384377 A, Accession: G69560 A/Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A, Molecule Type: DNA
A, Residues: 1-153 cKUN>
A, Cross-references: GB:299120; GB:AL009126; NID:g2635613; PIDN:CAB15288.1; PID:g2635795
A, Cross-references: GB:299120; GB:AL009126; NID:g2635613; PIDN:CAB15288.1; PID:g2635795
A, Chen, L.; Helmann, J.D.
Mol. Microbiol. 18, 295-300, 1995
A, Title: Bacillus subtilis MrgA is a Dps (PexB) homologue: evidence for metalloregulatio
A, Reference number: S70240; MVID:96296451; PMID:8709648
A, Accession: S70240
A, Status: preliminary; nucleic acid sequence not shown
A, Molecule type: DNA
A, Residues: 1-153 ccHE>
A, Cross-references: EMBL:L19547; NID:g852080; PIDN:AA68042.1; PID:g852076
B, Chen, L.; James, L.P.; Helmann, J.D.
A, Residues: 1-155, 5428-5437, 1993
A, Title: Metalloregulation in Bacillus subtilis: isolation and characterization of two A, Reference number: A48656; MVID:93374837; PMID:8396117
A, Residues: 1-60, WIPSLSAR, cCH2>
A, Cross-references: EMBL:Z22928; NID:g396219; PIDN:CAA80510.1; PID:g396221
B, Dowds, B.C.A.
Submitted to the Protein Sequence Database, February 1993
A, Reference number: A44519
A, Accession: D44519
A, Residues: 'X',2-15,'KST',19-20,'TVFRMH' < DOW>

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Gaps

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us-09-870-089b-9.rpr

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68.8%; Score 44; DB 2; Length 159; 62.5%; Pred. No. 8.1; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                 ilarity 62.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                           2 LHKWHWYV 9
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                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-498 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-554 <TAK>
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                      C;Genetics:
A;Gene: DR2142
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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C;Decies: Bacillus subtlis:
C;Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: H69618
C;Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: H69618
R;Kunst, F; Gasawara, N; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, R; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.Y; Caldwall, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Kochter, P.; Koningstein, G.; Krogh, S.; Rumano, M.; Kurita, K.; Lapduns, A.; Landinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maneda, S.; Maueell, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sekiguchi, J.; Sakowska, A.; Seror, A; Wuthors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sekiguchi, J.; Sakowska, A.; Seror, A; Wuthors: Yoshikawa, H.F.; Zumstein, R.; Yoshikawa, H.F.; Zumstein, R.; Yoshikawa, H.; Yamano, P.; Wipet, A.; Yamano, M.; Yamano, M.; Yata, K.; Yoshida, R.; A; Reference number: A69580; MUID:98044033; PMID:9384377; Propertium Bacillus subtilis.
A; Riccession: H69618
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(Species Deinococcus radiodurans

(Species Deinococcus radiodurans

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(Species Species S
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A;Cross-references: GB:AE002048; GB:AE000513; NID:g6459929; PIDN:AAF11686.1; PID:g645993
A;Experimental source: strain R1
A,Note: protein was found to over-accumulate in hydrogen peroxide-resistant mutant strai
C,Genetics:
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stress- and starvation-induced gene controlled by sigma-B dps - Bacillus subtilis
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0
                                                                                                                                                                                                                                     70.3%; Score 45; DB 2; Length 153; 75.0%; Pred. No. 5.5; vative 2; Mismatches 0; Indels
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C;Superfamily: hypothetical protein HI1349
                                                                                                                  A;Gene: mrgA
C,Superfamily: hypothetical protein HI1349
                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0%
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Best Local Similarity 75.v.
6, Conservative
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31 LHRFHWYV 38
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A;Status: preliminary
A;Molecule type: DNA
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C.Accession: 871751
R.Takahashi, M.; Inoue, N.; Ohishi, K.; Maeda, Y.; Nakamura, N.; Endo, Y.; Fujita, T.; 7
R.Takahashi, M.; Inoue, N.; Ohishi, K.; Maeda, Y.; Nakamura, N.; Endo, Y.; Fujita, T.; 7
R.Tatahashi, M.; Inoue, N.; Ohishi, K.; Maeda, Y.; Nakamura, N.; Endo, Y.; Fujita, T.; 7
A;Title: PIG-B, a membrane protein of the endoplasmic reticulum with a large lumenal dom A;Reference number: 871751; MUID:97015126; PMID:8861954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (EC 2.4.1.130) PIGB - ht N.Alternate names: membrane protein PIG-B; phosphatidyl-inositol glycolipid biosynthesis C;Species: Homo sapiens (man) C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Description: involved in surface protein binding to the membrane via glycosyl-phosphat A,Pathway: GPL-annchor blosynthesis C,Reywords: glycosyltransferase; haxosyltransferase; transmembrane protein P;60-77/Domain: transmembrane #status predicted <TMM>
dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase-like protein - Arabidope N;Alternate names: protein T913 150 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
                                                                                                                                                                          C)Accession: T51430
R)Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mewsubmitted to the Protein Sequence Database, August 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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A;Experimental source: cell line P39
A;Note: part of the genomic DNA was also sequenced
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 5
A;Introns: 78/2; 117/3; 152/3; 224/2; 318/2; 390/3; 441/2
A;Note: T9L3 150
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A,Experimental source: cultivar Columbia; BAC clone T9L3
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A;Accession: T51430
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1; Mismatches
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Matches 5; Conservative
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                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 LHOWHW 33
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                                                                                                              A;Accession: G82786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics;
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D
                                                                                                                                                                          General stress protein 20U [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: On May 2010 # sequence_revision 10-May-2001 # text_change 22-Oct-2001
C;Accesion: H90007
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
C; Sulba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H90007
A;Residues: preliminary
A;Rociale type: DNA
A;Residues: 1-147 <KUR>
A;Rociales: 1-147 <KUR>
A;Residues: 1-147 <KUR>
A;Residues: 1-147 <KUR>
A;Cross-references: GB:BA000018; PID:g13701933; PIDN:BAB43225.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A87628
A87628
Conserved hypothetical protein CG3059 [imported] - Caulobacter crescentus
conserved hypothetical protein CG3059 [imported] - Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: A87628
R;Nierman W.C.; Peldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A; Reference number: A87249; MUD:21173698; PMID:11259647
A; Reference number: A87249; MUD:21173698; PMID:11259647
A; Molecule type: DNA
A; Residues: 1-209 <STO>
A; Conserreferences: GB:AB005673; NID:g13424707; PIDN:AAK25021.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein XP0597 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
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83.3%; Pred. No. 15;
tive 1; Mismatches 0; Indels
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C,Superfamily: hypothetical protein H11349
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Matches 5; Conservative
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Best Local Similarity
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                                                     306 HPWHWY 311
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3 НКМНМУ 8
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C:Superfamily:
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C;Species: Streptomyces viridochromogenes
C;Date: 31-Mar-1992 #sequence_revision 26-Apr-1996 #text_change 19-May-2000
C;Accession: S20686; PT0060
C;Atligha, R.; Hillemann, D.; Nussbaumer, B.; Pelzer, S.; Wohlleben, W.
Submitted to the EMBL Data Library, March 1992
A;Description: Gene disruption and gene replacement analysis of a 4 kb BamHI fragment of a 4 kb BamHI frag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Status: preliminary
A.Molecule type: DNA
A.Molecule type: DNB
A.Molecule type: M.; Broer, I.; Hillemann, D.; Strauch, E.; Puehler, A.
A.Title: Nucleoide sequence of the phosphinothricin N-acetyltransferase gene from Stransference number: JT0409; MJID:89196914; PMID:3240868
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Réference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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A;Residues: 1-164 <MOH3>
A;Cross-references: GB:M22827; NID:g295177; PIDN:AAA72710.1; PID:g295180
A;Experimental source: strain Tue 494
C;Superfamily: probable lipolytic protein ybaC
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Pred. No. 16;
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alpha-amylase (BC 3.2.1.1) precursor [validated] - Bacillus licheniformis M.Alternate names: 1.4-alpha-D-glucan glucanohydrolase [5.5pecises Bacillus licheniformis C;5pecises D. 491997; B24549; B25454; B254
                                                                                                                                                                                         .....ss-reterences: EMBL:U58762; NID:g1330398; PID:g1330400; PIDN:AAB00719.1; GSPDB:GN0
A;Experimental source: strain Bristol N2; clone T27F7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Molecule type: DNA

A; Residues: 1-162, 'R', 164-512 < YUU>
A; Residues: 1-162, 'R', 164-512 < YUU>
A; Cross-references: GB: X30226; ND: G39551; PIDN: CAA26981.1; PID: G39552

A; Cross-references: ATCC 27811

B; Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt J: Bacteriol. 166, 635-643, 1986

A; Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearoth A; Reference number: A91817; MUID: 86195857; PMID: 3009417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 171, 2435-2442, 1989
A/Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-indepe
A/Reference number: I39773; MUID:89213924; PMID:2540150
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R;Hallsworth, K.
submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid T27F7.
A;Reference number: Z18613
A;Accession: T16945
                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DDB
A;Residues: 1.283 cHAL>
A;Cross-references: EMBL:U58762; NID:91330398; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                            65.6%; Score 42; DB 50.0%; Pred. No. 28; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                             A;Map position: 2
A;Introns: 11/1; 45/1; 63/1; 130/3; 248/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 50.0%; tes 4; Conservative
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143 VHPWYWYI 150
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Matches
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bialaphos acetylhydrolase - Streptomyces hygroscopicus
bialaphos acetylhydrolase - Streptomyces hygroscopicus
c;Species: Streptomyces hygroscopicus
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 17-Mar-2000
C;Accession: A47031
R;Raibaud, A.; Zalacain, M.; Holt, T.G.; Tizard, R.; Thompson, C.J.
J. Bacteriol. 173, 4454-4463, 1991
A;Title: Nucleotide sequence analysis reveals linked N-acetyl hydrolase, thioesterase,
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T1645
hypothetical protein T27F7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dete: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16945
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                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA.
A;Residues: 1-299 <RAI>
A;Residues: sequence extracted from NCBI backbone (NCBIN:41300, NCBIP:41303)
C;Superfamily: probable lipolytic protein ybaC
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Pred. No. 44;
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A;Reference number: A47031; MUID:91294191; PMID:2066341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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Pred. No. 21;
0; Mismatches
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1; Mismatches
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Similarity 71.4%;
5; Conservative
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Best Local Similarity 83.5
اتا 5، Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                         A; Status: preliminary
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A; Molecule type: DNA
A; Residues: 1-64;604-624 <VOL2>
R; Voit, R; Feldmaier-Fuchs, G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-624 < VOL>
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A; Residues: 1-624 <VOI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: 139756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: I39763
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A; Molecule typee DNA
A; Mosiduse typee DNA
A; Mosiduse typee DNA
A; Mosiduse typee DNA
A; Mosiduse typee DNA
A; Cross-references: GB:M65637; NID:g142498; PIDN:AMA22232.1; PID:g142499
B; Whn, H.; Fittack, P. P.; Lampen, J.O.
J. Bacreriol. 149, 372-373, 1982
A; Titae: N-Terminal amino acid sequence of Bacillus litcheniformis alpha-amylase: comparing the momber: A26151; MUD:82098050; PMID:6172418
A; Accession: A26151; MUD:82098050; PMID:6172418
A; Accession: A26151; MUD:82098050; PMID:6172418
A; Rosiduse: 30-37; E', 33-41, 'X', 43-47 < KUH>
A; Rosiduse: 30-37; E', 33-41, 'X', 43-47 < KUH>
A; Rosiduse: 30-37; E', 33-41, 'X', 43-47 < KUH>
A; Rosiduse: 30-37; E', 33-41, 'X', 43-47 < KUH>
A; Rosiduse: 30-37; E', 33-41, 'X', 43-47 < KUH>
A; Rosiduse: 30-37; E', 33-41, 'X', 43-47 < KUH>
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A; Rosiduse: 30-37; E', 33-41, 'X', 43-47 < KUH>
A; Rosiduse: 553788; MUD:95182462; PMID:7877175
A; Rosiduse: 553788; MUD:95182462; PMID:7877175
A; Rosiduse: 573788
A; Robinted to the Brookhave Protein bate Bank, July 1995
A; Robinted to the Brookhave Protein bate Bank, July 1995
A; Robinted to the Brookhave Protein bate Bank, July 1995
A; Robinted to the Brookhaven Protein bate Bank, October 1996
A; Robinted to the Brookhaven Protein Day C; Suh, S, M.
A; Robertiption: catalyzee the hydrolysis of internal 1,4-alpha-mylase core homology
C; Robinefis: amnotation; X-ray crystallography, 1.7 angstroms, residues 32-210;222-511
C; Geneeis: amnotation; X-ray crystallography, 1.7 angstroms, Residuses; Polysacc
A; Robinefised to the Brookhaven Protein para Bank, October 1996
A; Robertiption: catalyzee the hydrolysis of internal 1,4-alpha-mylase polysacc
C; Roynords: extracellulat protein; Glycosidase heat-stable protein; Hydrolysis of Status predicted extra
C; Robinefish H; Salpha-amylase amylase esterimental experimental
F; 2500, 290, 2549 Binding site: calcium
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N'Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus amyloliquefaciens
C;Species: Bacillus amyloliquefaciens
C;Accession: A92389; A90307; Ī39756; I39763; A00843
R;Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, I. Biol. Chem. 258, 1007-1013, 1983
A;Title: Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced fr A;Reference number: A92389; MUID:83108808; PMID:6185474
A, Molecule type: DNA
A, Residues: 1-29 < LAO>
A, Third B. L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A, Thirle: In vivo genetic engineering: homologous recombination as a tool for plasmid con A, Reference number: 139772; MUID: 91092499; PMID: 2265757
A, Accession: 139772
A, Status: translated from GB/EMBL/DDBJ
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A, Molecule type: DNA
A, Residues: 1-514 <TAK>
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A,Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
R;Ruobonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, S.
Gene 59, 161-170, 1987
A;Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amylase cells by its careference number: 139763; MUID:88137952; PMID:2830166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Voll, W.; Voit, R.
Proc. Natl. Acad. Sci. U.S.A. 87, 5312-5316, 1990
A;Title: Characterization of the gene encoding the hemocyanin subunit e from the tarant A;Reference number: A35772; MUID:90319102; PMID:2371273
A;Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA2: R;Chung, H.S.; Friedberg, F. Biochem. J. 185, 387-395, 1980
A;Tittle: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amylase. A;Reference number: A90307; MUID:80241725; PMID:6156671
                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A;Residues: 32-53, I',55-63, L',65-78, D',80-83, S',85-222 <CHU>
R;Palva, L; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H
A;Pile. 15, 1981
A;Tille: Mucleotide sequence of the promoter and NH2-terminal signal peptide region of
A;Reference number: 139756; MUID:82051296; PMID:6170539
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A;Title: Arthropod hemcoyanins. Molecular cloning and sequencing of cDNAs encoding the A;Reference number: A37975; MUID:91060544; PMID:2246235
A;Accession: S13441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-31/Domain: signal sequence #status predicted <BIO>
F;32-514/Product: alpha-amylase #status predicted <MPT>
F;229-362/Domain: alpha-amylase core homology <AMY>
F;239-362/Binding site: calcium (Asn, Asp, His) #status predicted
F;262,292,359/Active site: Asp, Glu, Asp #status predicted
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C;Species: Burypelma californica
C;Date: 15-Nov-1984 #sequence revision 31-Mar-1992 #text change 22-Jun-1999
C;Accession: S06701; A35772; Š13441; A02566; A24179; B37975; S08107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-39 <RE2>
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A;Reference number: S06701
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A;Molecule type: DNA
A;Residues: 1-96 <RES>
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A;Cross-references: EMBL:X16894; NID:99268; PIDN:CAA34772.1; PID:99269
R;Schneider, H.J.; Drexel, R.; Feldmaier, G.; Linzen, B.; Lottspeich, F.; Henschen, A. Hopte-Seyler's Z. Physiol. Chem. 364, 135-1381, 1983
A;Title: Hemocyanins in solders, X111[81]. Complete amino-acid sequence of subunit e from A;Reference number: A02566; MUID:84059635; PMID:6357986
A;Accession: A02566; MUID:84059635; PMID:6357986
A;Molecule type: protein
A;Residues: 2.29, 'R', 31-46,'D', 48-79,'K', 81-90,'H', 92-110,112-159,'K', 161-216,'H', 218-25
C;Superfamily: hemocyanin
C;Reywords: copper; hemocyanin c #status experimental <MAT>
F;2-150/Domain: 1 < D00.>
F;2-150/Domain: 1 < D00.>
F;3-150/Domain: 3 < D00.>
F;35-624/Pondiut: 3 < D00.>
F;35-624/Domain: 3 < D00.>
F;350/Shinding site: copper (His) #status predicted
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Search completed: December 16, 2003, 14:19:17 Job time : 11.3333 secs

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P00292 bacillus am
P02242 curypelma c
P80476 androctonus
Q91f15 curypelma c
P22383 simian immu
C00254 homo sapien
C00255 simian immu
C001251 accharomyc
C00139 saccharomyc
C01315 caenorhabdi
P16665 treponema p
P17915 treponema p
C01318 mocracla s
P47074 saccharomyc
C01184 curypelma c
C01184 coprinus ci
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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PEDI CABEL
PEDI CABEL
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SPSG-BACSU
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Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.; "Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rrnB-dnaB region.";
                                                                                                                                                                                                                                                                      OXIDATIVE KILLING.
INDUCTION: BY OXIDATIVE STRESS AND BY GROWTH IN MINIMAL MEDIUM
LACKING IRON (FE-III), OR ONE OF THE DIVALENT CATIONS MANGANESE,
                                                                                                                                                               Chen L., Helmann J.D.;
"Bacillus subtilis MrgA is a Dps(PexB) homologue: evidence for
"Bacillus subtilis MrgA is a oxidative-stress gene.";
mot. Microbiol. 18:295-304.

-i- FUNCTION: FORMS HIGHLY STABLE, MULTIMERIC PROTEIN-DNA COMPLEXES
WHICH ACCUMULATE IN STATIONARY-PHASE CELLS AND PROTECT AGAINST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.3%; Score 45; DB 1; Length 153; 75.0%; Pred. No. 3.4; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      General stress protein 20U (GSP20U) (DPS protein homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Complete_protecome.
153 AA; 17332 MW; 3082CF803401E17D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 AA.
                                                                                                                                                                                                                                                                                                                                              -! - SIMILARITY: BELONGS TO THE DPS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98048467; PubMed=9387221;
                                                                                                                             CHARACTERIZATION.
MEDLINE=96296451; PubMed=8709848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L19547; AAA68042.1; -.
EMBL; Z22928; CAA80510.1; -.
EMBL; Z93941; CAB07970.1; -.
EMBL; Z99120; CAB15288.1; -.
PIR; G69660; G69660.
Subtilist; BG10864; mrgA.
InterPro; IPR001217; DPS.
InterPro; IPR001519; Ferritin.
Pfam; PF00210; ferritin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01346; HELNAPAPROT.
ProDom; PD149803; DPS; 1.
PROSITE; PS00818; DPS 1; 1.
PROSITE; PS00819; DPS_2; 1.
                                                                                             Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 75.0
es 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||::||||
31 LHRFHWYV 38
                                                                                                                                                                                                                                                                                                                               COPPER OR COBALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LHKWHWYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G20U BACSU
ID G20U BACSU
AC P80879;
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Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursler L., Brans A., Braun M., Brigall S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Korita K., Lapidus A., Liu H., Masuda S., Mauel C., Madiau C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Mediau C.,
RA Medina N., Mellado R.P., Mizuno M., Mosetl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Satro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Sekiguchi J., Sekowska A., Seron S.J., Seror P., Shin B.S., Soldo B.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Takamashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Taraptra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Taraptra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Taraptra P., Vasamotc K., Yata K.,
Whiters P., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wambutter R., Wedler E., Wedler H., Wantaers P., Wanther R., Paramile E., Schleier E., Wedler H., Wantaers P., Wanther R., Paramile E., Bohlier E., Wedler E., Wedler H., Wantaers P., Wantaerte P., Wantaerce Of the Gram-positive bacterium Bacillus
F. Thill H. Wantaer E., Wantaer C. E., Carlon E.,
RA Toshida K., Yoshikawa H.F., Zuma-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "First steps from a two-dimensional protein index towards a response-
regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
-!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE
LIMITATION AND OXYGEN LIMITATION.
-!- SIMILARITY: BELONGS TO THE DPS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97443988; PubMed-9298659;
Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 AA; 16462 MW; 21ADBC4438E5E3E2 CRC64;
                                                                                                MEDLINE=98044033; PubMed=9384377;
Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF008220; AAC00237.1; -.
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INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, 299119; CAB15043.1; ... PIR; H65618; H69618.
Subtilist; BG12584; dps.
InterPro; IRR002177; DpS.
InterPro; IPR001519; Ferritin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01346; HELNAPAPROT.
PRODOM; PD14963; DPS; 1.
PROSITE; PS000818; DPS; 1; 1.
PROSITE; PS000819; DPS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00210; ferritin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 390:249-256(1997).
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                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-14.
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68.8%; Score 44; DB 1; Length 144;

Query Match

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SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT:
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P14750;
                                                                                                                                                                                                                                   subunits.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 21705;
MEDLINE=91294191; PubMed=2066341;
MEDLINE=91294191; PubMed=2066341;
Raibaud A., Zalacain M., Holt T.G., Tizard R., Thompson C.J.;
Raibaud A., Zalacain M., Holt T.G., Tizard R., Thompson C.J.;
"Nucleotide sequence analysis reveals linked N-acetyl hydrolase,
thiosesterase, transport, and regulatory gense encoded by the
bialaphos biosynthetic gene cluster of Streptomyces hygroscopicus.",
J. Bacteriol. 173:4454-4463(1991).
-!- FONCTION: THIS PROTEIN REMOVES THE N-ACETYL GROUP FROM
BIALAPHOS AS ONE OF THE FINAL STEPS OF THE BIALAPHOS
BIOSYNTHETIC PATHWAY.
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: Bialaphos biosynthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.2%; Score 43; DB 1; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4265C8E6E10FAE97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Acetyl-hydrolase (EC 3.1.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hemocyanin C chain (HcC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        628 AA
75.0%; Pred. No. 4.5; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eurypelma californica (American tarantula).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, M64783, AAA79277.1; -.
InterPro, IPR002168; Lipolytic_enzyme.
InterPro, IPR000379; Ser_effrs_eite.
PROSITE, PS01173; LIPASE_GDXG_HIS, 1.
PROSITE; PS01174; LIPASE_GDXG_SER: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase, Antibiotic biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 AA; 32096 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces hygroscopicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                             6; Conservative
                                                                                                                                                                                                                                 STANDARD;
                                                                                                22 LHNYHWYV 29
    Best Local Similarity
                                                                      2 LHKWHWYV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Q9NFL6;
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Q01109;
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ACT SITE
SEQUENCE
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                                                                                                                                                                                                            Voit R., Feldmaler-Puchs G., Schweikardt T., Decker H., Burmester T.; "Complete sequence of the 24-mer hemocyanin of the tarantula Burypelma californicum. Structure and intramolecular evolution of the
                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 275:39339-39344 (2000).
-!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN
DIFFERENT CHAINS IDENTIFIED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SÜBCELLULAR LOCATION: Extracellular.
-1- TISSUB SPECIFICITY: Hemolymph.
-1- TISSUB SPECIFICITY: Hemolymph.
-1- MISCELLABOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN
LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A
BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN
ADDITION TO BINDING OXYGEN.
-1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Aphonopelma.
NCBI TaxID=29932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC, .) (POTENTIAL).
N-LINKED (GLCNAC, .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                            TISSUE=Heart;
MEDLINE=20564303; PubMed=10961996;
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HSSP; P04253; ILLA.
INTERFO, IPR000896; Hemocyanin.
INTERPO; IPR005203; hemocyanin.C.
INTERPO; IPR005204; hemocyanin.N.
INTERPO; IPR00527; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00209; HEMOCYANIN 1; 1. PROSITE; PS00210; HEMOCYANIN 2; 1. PROSITE; PS00498; TYROSINASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00372; hemocyanin; 1.
Pfam; PF03723; hemocyanin C; 1.
Pfam; PF03722; hemocyanin N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
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INIT MET 0 0 0
DISULFID 536 584
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                                                                                                                             SEQUENCE FROM N.A.
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Gaps

Indels

1;

Pred. No. 24; 1; Mismatches

71.4%;

Conservative

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Best Local Similarity
                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91025623; PubMed=2222854; Schartau W., Metzger W., Sonner P., Geisert H., Storz H.; Schartau W., Metzger W., Sonner P., Geisert H., Storz H.; "Hemocyanins in spiders, XXIII. Complete amino-acid sequence of subunit a of Eurypelma californicum hemocyanin."; Biol. Chem. Hoppe-Seyler 371:557-565[1990].

-i. Function: HEMOCYANING ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFIED.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECITY: Hemolywark.
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COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
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MISCELLANEOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN
LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A
BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN
ADDITION TO BINDING OXYGEN.
SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                                                                                                                                                                               sequencing of cDNAs
                                                                                                        Eurypelma californica (American tarantula).
Eukaryota, Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Aphonopelma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxygen transport; Copper; Glycoprotein; Hemolymph.
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                                                                                                                                                                                                                                                                                                                    Voit R., Feldmaier-Fuchs G.;
"Arthropod hemocyanins. Molecular cloning and sequenc:
encoding the tarantula hemocyanin subunits a and e.";
J. Biol. Chem. 265:19447-19452(1990).
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      01-NOV-1990 (Rel. 16, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
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InterPro; IPR005203; hemocyanin_C.
InterPro; IPR005204; hemocyanin_N.
InterPro; IPR005204; hemocyanin_N.
InterPro; IPR005227; Tyrosinase.
Pfam; PP00372; hemocyanin_I.
Pfam; PP03722; hemocyanin_I.
PRINTS; PR00187; HABMOCYANIN.
PROSITE; PS00209; HEMOCYANIN_I.
PROSITE; PS002109; HEMOCYANIN_I.
PROSITE; PS00210; HEMOCYANIN_I.
                                                                                                                                                                                                                                                                                        MEDLINE=91060544; PubMed=2246235;
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HSSP; P04253; 1LLA.
                                                       Hemocyanin A chain (HcA).
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SEQUENCE FROM N.A.
                                                                                                                                                                                                           NCBI_TaxID=29932;
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Score 43; DB 1; Length 630;

67.2%;

Query Match

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STRAIN=ATCC 27811;
MEDLINE=86111694; PubMed=2418011;
Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
Tsukagoshi N., Udaka S.,
"Complete nucleotide sequence of a gene coding for heat- and
pH-stable alpha-amylase of Bacillus licheniformis: comparison of the
amino acid sequences of three bacterial liquefying alpha-amylases
deduced from the DNA sequences.";
J. Biochem. 98:1147-1156(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-84185455; PubMed-6609154; Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.; Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.; Incheside sequence of the 5' region of the Bacillus licheniformis alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89213224; PubMed=2540150;
Laoide B.M., Chambliss G.H., McConnell D.J.;
Bacillus licheniformis alpha-amylase gene, amyL, is subject to
promoter-independent catabolite repression in Bacillus subtilis.";
J. Bacteriol. 171:2415-2442(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                       Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L., Carmona C., Requadt C.;
"Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus and Bacillus licheniformis.";
J. Bacteriol. 166:635-643(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-amylase: comparison with Bacillus amyloliquefaciens and Bacillus subtilis Enzymes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 30-47.

MEDIJURE=82098050 P. P., Lampen J.O.;

Kuhn H., Fieterzek P.P., Lampen J.O.;

"N-terminal amino acid sequence of Bacillus licheniformis
                                                              01-JAN-1988 (Rel. 06, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-amylase precursor (BC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                              Bacillus licheniformis.
Bacteria, Pirmicutes; Bacillales; Bacillaceae, Bacillus
                 512 AA
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                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86195857; PubMed=3009417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol. 158:369-372(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol, 149:372-373(1982).
                                                01-JAN-1988 (Rel. 06, Created)
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                   STANDARD;
                                                                                                                    qlucanohydrolase).
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                 AMY BACLI
P06278;
AMY BACLI
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                                                                                                                                                                                                                                                                                                            PRINTS; PRO0110; ALPHAAMYLASE.
SWART; SW00642; Aamy; 1.
Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; 3D-structure.
1. 29
                NOVOZYMĖS.
MISCELLANEOUS: ABLE TO WORK AT RELATIVELY HIGH (ALKALINE) PH
VALUES (UP TO PH 11) AND AT HIGH TEMPERATURES (UP TO 100 DEGREE
                                                SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
liquefaction of starch-containing mashes and in the detergent industry to remove starch. Sold under the name Termamyl by
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C -> Y (IN REF. 5
R -> L (IN REF. 5
S -> G (IN REF. 2
S -> G (IN REF. 2
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PDB; 1BPL; 17, A106-96.
PDB; 1BL; 23-MAR-97.
PDB; 1E3X; 21-JUN-01.
PDB; 1E3X; 21-JUN-01.
PDB; 1E43; 21-JUN-01.
PDB; 1E43; 21-JUN-01.
PDB; 1D80; 30-JAN-03.
InterPro; IPR0066589; Alp amyl_cat_sub.
InterPro; IPR006646; Alpha_amyl_cat.
InterPro; IPR006646; Alpha_amyl_cat.
Pfam; PF00128; Alpha_amylase: 1.
                                                                                                                                                      EMBL, M38570; AAA2226.1; --
EMBL, M1326; AAA2226.1; --
EMBL, K01984; AAA22193.1; --
EMBL, M26412; AAA2237.1; --
EMBL, A17930; CAA01355.1; --
PIR, A91997; ALBSL.
PDB, 18PL, 17-AUG-96.
                                                                                                                                               EMBL; X03236; CAA26981.1; -.
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PD0692,
21-JUL-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58549 MW; D8BB77759CD4C482 CRC64;
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Best Local Similarity 100.
Matches 5; Conservative
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512 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; 3D-structure.
                                                                                        "Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced from the nucleotide sequence of the cloned gene."; J. Biol. Chem. 258:1007-1013(1983).
                                                                                                                                                  SEQUENCE OF 32-222.
MEDLINE-80241725; PubMed-6156671;
"Chung H.S., Friedberg F."
"Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
                                                                                                                                                                                                                                                           MEDINE-82051296; PubMed-6170539;
Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M., Soederlund H., Takkinen K., Kaeaeriaeinen L.;
"Nucleotide sequence of the promoter and NH2-terminal signal peptide region of the alpha-amylase gene from Bacillus amyloliquefaciens.";
Gene 15:43-51(1981).
                                                                                                                                                                                                                                                                                                                                                       MEDLINE-83108808; PubMed-6185474;
Takkinen K., Pettersson R.F., Kalkkinen N., Palva I., Soederlund H.,
Kaeaeriaeinen L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.6%; Score 42; DB 1; Length 514; 100.0%; Pred. No. 28;
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BY SIMILARITY.

L -> 1 (IN REF. 2).

I -> 5 (IN REF. 2).

G -> 5 (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR006589; Alp amyl_cat_sub. Interpro; IPR006604; Alpha amyl_cat. Pfam, PF00128; alpha-amylase; 1. SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                     31ochem. J. 185:387-395(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58403 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, JO1542; AAA22191.1; -. EMBL, V00092; CAA23430.1; -. EMBL, AZ0154; CAA01489.1; -. EMBL; M18424; AAA22192.1; -.
                                                                                                                                                                                                                                                SEQUENCE OF 1-96 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1E3X; 21-JUN-01.
PDB; 1E3Z; 21-JUN-01.
PDB; 1E40; 21-JUN-01.
PDB; 1E43; 21-JUN-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         514 AA;
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                              SEQUENCE FROM N.A.
  NCBI_TaxID=1390;
                                                                                                                                                                                                           amylase."
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide sequence corresponding to subunit e.";

Bur. J. Biochem. 159:23-29 (1986)

-i- FUNCTION: HEMOCYANING ARE COPER-CONTAINING OXYGEN CARRIERS

OCCURRING PREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                         Voll W., Voit R.; "Characterization of the gene encoding the hemocyanin subunit e from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-84059635; PubMed=6357986;
Schneider H.-J., Drexel R., Feldmaier G., Linzen B., Lottspeich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFIED.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: HEMOLYMPh.
-!- MISCELLANEOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN LIGANDS (PRESIDURE) SY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.
-!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 74-599 FROM N.A.
MEDLINE=86300721; PubMed=3017715;
Voit R., Schneider H.-J.;
"Tarantula hemocyanin mRNA. In vitro translation, cDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Voit R., Feldmaier-Fuchs G.;
"Arthropod hemocyanins. Molecular cloning and sequencing of cDNAs encoding the tarantula hemocyanin subunits a and e.";
J. Biol. Chem. 265:19447-19452(1990).
                                                                                                                                                                                                                                                                     Burypelma californica (American tarantula).
Bukaryota, Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Aphonopelma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Henschen A.; "Hemcyanins in Spiders, XVIII. Complete amino-acid sequence of subunit e from Eurypelma californicum hemocyanin."; Hoppe-Seyler's Z. Physiol. Chem. 364:1357-1381(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     the tarantula Eurypelma californicum.";
Proc. Natl. Acad. Sci. U.S.A. 87:5312-5316(1990).
                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
01-APR-1990 (Rel. 14, Last sequence update)
48-FBR-2003 (Rel. 41, Last annotation update)
Hemocyanin E chain (HCE).
                                                                                                                                      623 AA.
                                                                                                                                      PRT;
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                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                       183 KWHWY 187
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 MCBI_TaxID=29932;
4 KWHWY 8
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                                                                                                                                      HCYE EURCA
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"Complete amino acid sequence of the Aa6 subunit of the scorpion
Androctonus australis hemocyanin determined by Edman degradation and
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hemocyanin F chain (HcF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.6%; Score 42,
57.1%; Pred. No. 33;
+ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 628 AA.
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Best Local Similarity 57.1.
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                        mass spectrometry."
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                                                                      ARTHROPODS.
                                                                                                                                                                                                              SUBFAMILY.
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HCYF_EURCA
ID HCYF_EURCA
AC Q9NFL5;
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SEQUENCE
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Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

Buthoidea; Buthidae; Androctonus.
                                                                                                         R InterPro; IPR005203; hemocyanin.
R InterPro; IPR005203; hemocyanin.
R InterPro; IPR005203; hemocyanin.
R InterPro; IPR005227; Tyrosinase.
R Edan; PF00372; hemocyanin; 1.
R Pfam; PF03723; hemocyanin; 1.
R PROSITE; PS00210; HEWOCYANIN 1; 1.
R PROSITE; PS00210; HEWOCYANIN 2; 1.
R PROSITE; PS00499; TYROSINASE_2; 1.
R TAINSport; Oxygen transport; Copper; Glycoprotein; Hemolymph.
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C -> D (IN REF. 2).
R -> K (IN REF. 2).
A -> H (IN REF. 2).
MISSING (IN REF. 2).
K -> R (IN REF. 2).
K -> R (IN REF. 2).
K -> R (IN REF. 2).
K -> H (IN REF. 2).
H -> M (IN REF. 2).
C -> H (IN REF. 2).
C -> M (IN REF. 2).
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MEDLINE=56061936; PubMed=7588779;
Buzy A., Gagnon d., Lamy J., Thibault P., Forest E.,
Hudry-Clergeon G.;
                                                                                                                                                                                                                                                        COPPER 1 (PROBABLE).
COPPER 1 (PROBABLE).
COPPER 1 (PROBABLE).
                                                                                                                                                                                                                                                                                             (PROBABLE).
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V -> P (IN REF. 3).
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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COPPER 2 (PROBA
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COPPER 2 (PROBA
COPPER 2 (PROBA
BY SIMILARITY.
N-LINKED (GLCNA
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         EMBL; X16651; CAA34643.1; JOINED. EMBL; X16652; CAA34643.1; JOINED. EMBL; X16653; CAA34643.1; JOINED. EMBL; X16655; CAA34643.1; JOINED. EMBL; X16655; CAA34643.1; JOINED. EMBL; X16656; CAA34643.1; JOINED. EMBL; X16666; CAA34643.1; JOINED. EMBL; X16667; CAA34643.1; JOINED. EMBL; X16657; CAA34643.1; JOINED. EMBL; X16657; CAA34643.1; JOINED. EMBL; S16677; CAA34643.1; JOINED. EMSP; PO4253; JOXY.
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  X16650; CAA34643.1; -.
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623 AA;
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P80476;
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CONFLICT
CONFLICT
SEQUENCE
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DISULFID
CARBOHYD
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HCY6_ANDAU
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TISSUE=Heart;
MEDLINE=205643103; PubMed=10961996;
Woit R., Feldmaier-Fuchs G., Schweikardt T., Decker H., Burmester T.;
"Complete sequence of the 24-mer hemocyanin of the tarantula Eurypelma californicum. Structure and intramolecular evolution of the
                                                                                                 ATHOROGOMES

-1- SUBUNIT: SCORPION HEMOCYANIN IS A 24-CHAIN POLYMER WITH 8

DIFFERENT CHAINS IDENTIFIED, ASSEMBLED IN HEXAMERIC SUBSTRUCTURES.
-1- SUBCELLULAR LOCATION: Extracellular.
-1- TISSUB SPECIFICITY: Hemolymph.
-1- PTM: THREE DISULFIDE BONDS ARE PRESENT.
-1- MASS SPECIFICAMERY: MW=71890; MW ERR=7; METHOD=Electrospray.
-1- MISCELLANDOUS: THE TWO COPPER IONS BOUND BACH HAVE 3 NITROGEN LIGAND (POSSIBLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.
-1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Bur. J. Blochem. 233:93-101(1995).
-1- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burypelma californica (American tarantula).
Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Mygalomorphae, Theraphosidae, Aphonopelma.
MCBI_TaxID=29932;
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174 COPPER 1 (PROBABLE).
201 COPPER 2 (PROBABLE).
321 COPPER 2 (PROBABLE).
325 COPPER 2 (PROBABLE).
374 PHOSPHORYLATION (PROBABLE).
374 PHOSPHORYLATION (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 1; Length 626;
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HSSP; P04253; 10XY.
InterPro; IPR000896; Hemocyanin.
InterPro; IPR000503; hemocyanin.
InterPro; IPR005204; hemocyanin.
InterPro; IPR005204; hemocyanin.
InterPro; IPR002207; Tyrosinase.
Pfam; PP03722; hemocyanin.
Pfam; PP03722; hemocyanin.
Pfam; PR03722; hemocyanin.
Pfam; PR03722; hemocyanin.
PROSITE; PS00209; HEMOCYANIN.
PROSITE; PS00210; HEMOCYANIN.
PROSITE; PS00210; HEMOCYANIN.
PROSITE; PS00498; TYROSINASE_2; I.
Transport; Oxygen transport; Copper; Hemolymph;
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Biol, Chem. 275:39339-39344(2000).
- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                          COPPER 1 (BY SIMILARITY).
COPPER 1 (BY SIMILARITY).
COPPER 1 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
COPPER 3 (BY SIMILARITY).
COPPER 4 (BY SIMILARITY).
COPPER 5 (BY SIMILARITY).
COPPER 6 (GLCNAC. . ) (POTENTIAL).
N.LINKED (GLCNAC. . ) (POTENTIAL).
N.LINKED (GLCNAC. . ) (POTENTIAL).
                                         SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN
                                                0;
                                                                                                                                                                                                                                                                                                                                                                           Copper; Glycoprotein; Hemolymph. BY SIMILARITY. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.6%; Score 42; DB 1; Length 628; 57.1%; Pred. No. 33; 1; Indels Live 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virion infectivity factor (SOR protein) (Q protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simian immunodeficiency virus (isolate GB1).
                                                                                                                                                                                                                                                                 INGERPO, IPRO00896; Hemocyanin, InterPro; IPRO05203; hemocyanin, InterPro; IPRO05204; hemocyanin, InterPro; IPRO05204; hemocyanin, N. InterPro; IPRO05227; Tyrosinase. Pfam, PF00372; hemocyanin, 1. Pfam, PF03722; hemocyanin, N. PROSITE; PS002109; HEMOCYANIN 1; 1. PROSITE; PS002109; HEMOCYANIN 1; 1. PROSITE; PS002109; HEMOCYANIN 1; 1. PROSITE; PS002109; HEMOCYANIN 2; 1. Transport; Oxygen transport; Copper; INIT MET MET S33 581 BY SIMII
                                                                                                                                                                                                                                               EMBL; AJ277491; CAB89496.1; -.
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Best Local Similarity 57.1.
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171
171
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202
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446
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628 AA;
                                                                                                                                                                                                                                                         P04253; 1LLA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=11732;
                                ARTHROPODS
                                                                                                                                        SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIF_SIVGB
P22383;
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                       Tsujimoto H., Hasegawa A., Maki N., Fukasawa M., Miura T., Speidel S.,
Cooper R.W., Moriyama E.N., Gojobori T., Hayami M.;
"Seguence of a novel simian immunodeficiency virus from a wild-caught
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANTS SER-15; VAL-177 AND ASP-250. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Foel C.L., Yi Q., Nickerson D.A.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schmidt V.A., Nierman W.C., Maglott D.R., Cupit L.D., Moskowitz K.A., Wainer J.A., Bahou W.F.;
"The human proteinase-activated receptor-3 (PAR-3) gene.
Identification within a PAR gene cluster and characterization in vascular endothelial cells and platelets.";
J. Biol. Chem. 273:15061-15068(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Proteinase activated receptor 3 precursor (PAR-3) (Thrombin receptor-like 2) (Coagulation factor II receptor-like 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97242411; PubMed=9087410;
Ishihara H., Connolly A.J., Zeng D., Kahn M.L., Zheng Y.-W.,
Timmons C., Tram T., Coughlin S.R.;
"Protease-activated receptor 3 is a second thrombin receptor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.5%; Score 40; DB 1; Length 172;
62.5%; Pred. No. 20;
live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND MUTAGENESIS OF THR-39 AND PHE-40.
                                                                                                                                                                               Nature 341:539-541(1989).
-!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
-!- MISCELLANEOUS: THIS IS AN AFRICAN MANDRILL ISOLATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 172 AA; 20499 MW; 205E7BDDE6265FCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M27470; AAB49570.1; -.
InterPro; IPR000475; Viral_infect.
Dam, PP00559; VIf; 1.
PRINTS; PR00349; VIRIONINFECT.
ProDom; PD000063; Viral_infect; 1.
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MEDLINE=90015168; PubMed=2797181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 62.5
Les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LHKWHWYV 9
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                                                                                                                                                    African mandrill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F2RL2 OR PAR3
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PAR3 HUMAN
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MEDLINE=99178892; PubMed=10079109;

PUNCTION

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                                                                                                                                                                                                                                                                                                                        MIM, 601919; ...
Go; Go:0005887; F:thrombin receptor activity; TAS.
Go; Go:0015057; F:thrombin receptor activity; TAS.
Go; Go:0007526; P:blood coagulation; TAS.
Go; Go:0007229; P:phosphatidylinositol-4,5-bisphosphate hydro. ..; TAS.
Go; Go:0009611; P:response to wounding; TAS.
InterPro; IPR000276; GPRR Rhodpsn.
PEAM; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPRRINDOPSN.
PROSITE: PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE: PS05262; GPROTEIN RECEP F1 2; 1.
PROSITE: DS0562; GPROTEIN RECEP F1 2; 1.
                   7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMOVED FOR RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F->A: ALTERED SIGNAL UPON THROMBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T->P: NO PROTEOLYTIC CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEINASE ACTIVATED RECEPTOR 3.
Kahn M.L., Nakanishi-Matsui M., Shapiro M.J., Ishihara H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blood coagulation; Polymorphism.
                                                                                                                                                                                                                                                                        EMBL; U92971; AAC51218.1; -.
EMBL; AF374726; AAK51564.1; -.
HSSP; P34996; IDDD.
                                                                                                                                                                                                                                                                                                             Genew; HGNC:3539; F2RL2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Voit R., Feldmaier-Fuchs G., Schweikardt T., Decker H., Burmester T.; "Complete sequence of the 24-mer hemocyanin of the tarantula Burypelma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 275:39339-39344 (2000).
-I. FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING PREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFIED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUB SPECIFICITY: Hemolymph.
-!- TISSUB SPECIFICITY: Hemolymph.
-!- MISCELLANEOUS: THE TWO COPPER LOWS BOUND EACH HAVE 3 NITROGEN LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.
-!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Mygalomorphae, Theraphosidae, Aphonopelma.
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0
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PROSITE; PS00210; HEMOCYANIN 1; 1.
PROSITE; PS00498; TYROSINASE 2; 1.
Transport; Oxygen transport; Copper; Glycoprotein; Hemolymph.
INIT MET 0 0 BY SIMILARITY.
DISULFID 533 581 BY SIMILARITY.
COPPER 1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  californicum. Structure and intramolecular evolution of the
                                                  62.5%; Score 40; DB 1; Length 374; 71.4%; Pred. No. 40;
                                                                                          1; Indels
              374 AA; 42508 MW; C45C15A695DD1ABB CRC64;
                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                Eurypelma californica (American tarantula).
                                                                        Pred. No. 40;
1; Mismatches
CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ290429; CAB89498.1; -.
HSSP; P04253; ILLA.
InterPro; IPR000896; Hemocyanin.
InterPro; IPR005203; hemocyanin.C.
InterPro; IPR005204; hemocyanin.N.
InterPro; IPR002277; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20564303; PubMed=10961996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00372; hemocyanin; 1.
Pfam; PF03723; hemocyanin C; 1.
Pfam; PF03722; hemocyanin N; 1.
                                                                        Local Similarity 71.4
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                          Hemocyanin B chain (HcB).
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                    294 HRWLWYV 300
                                                                                                                                3 HKWHWYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=29932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Heart
                                                                                                                                                                                                                                                              HCYB EURCA
Q9NFH9;
                    SEQUENCE
                                                        Query Match
                                                                                                                                                                                                                            RESULT 13
HCYB EURCA
                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schartau W., Eyerle F., Reisinger P., Geisert H., Storz H., Linzen B., "Hemcoyanins in spiders, XIX. Complete amino-acid sequence of subunit d from Eurypelma californium hemcoyanin, and comparison to chain e."; Hoppe-Seyler's Z. Physiol. Chem. 364:1383-1409(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Heart;
MEDLINE-20564303; PubMed=10961996;
MEDLINE-20564303; PubMed=10961996;
Voit R., Feldmaier-Fuchs G., Schweikardt T., Decker H., Burmester T.;
"Complete sequence of the 24-mer hemocyanin of the tarantula Eurypelma
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 275:39339-39344 (2000).
-!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBGLIANT TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN DIFFERENT CHAINS IDENTIFIED.

BUBCELLULAR LOCATION: Extracellular.

ISSUE SPECIFICITY: Hemolymph.

MISCELLANGOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.

SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
COPPER 1 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
COPPER 2 (BY SIMILARITY).
N-LINKED (GLONAC. . ) (POTENTIAL).
N-LINKED (GLONAC. . .) (POTENTIAL).
17 1764FB28C91F9974 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eurypelma californica (American tarantula).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              californicum. Structure and intramolecular evolution of the
                                                                                                                                                         62.5%; Score 40; DB 1; Length 626;
                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                          HCYD_EURCA STANDARD; PRT; 626 AA. P02241; CONFH8; 21-JUL-1996 (Rel. 01, Created) 26-CT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                        64;
                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Chelicerati
Mygalomorphae; Theraphosidae; Aphonopelma.
NCBI_TaxID=29932;
 COPPER 1
COPPER 2
COPPER 2
COPPER 2
COPPER 2
                                                                                     N-LINKED
N-LINKED
                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=84059636; PubMed=6642428;
                                                                                                                        71966 MW;
                                                                                                                                                                           57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                Hemocyanin D chain (HcD).
                                                                                                                                                                                          Conservative
                203
323
327
363
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InterPro; IPR000896; Hemocyanin. InterPro; IPR005203; hemocyanin\_C.

EMBL; AJ290430; CAB89499.1; -.

P04253; 1LLA.

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Nakashima H., Behrens P.O., Moore M.D., Yokota E., Riggs A.F.; "Structure of hemocyanin II from the horseshoe crab, Limulus polyphemus. Sequences of the overlapping peptides, ordering the CNBr Eragments, and the complete amino acid sequence."; J. Biol. Chem. 261:10526-10533(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota, Metazoa, Arthropoda, Chelicerata, Merostomata, Xiphosura,
Limulidae, Limulus.
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   InterPro; IPR002227; Tyrosinase.
Pfam; PF00372; hemocyanin, 1.
Pfam; PF00372; hemocyanin, 2, 1.
Pfam; PF0722; hemocyanin, 2, 1.
PRINTS; PR00187; HAEMOCYANIN, 1.
PROSITE; PS00209; HEMOCYANIN, 1.
PROSITE; PS00499; TYROSINASE_2; 1.
PROSITE; PS00499; TYROSINASE_2; 1.
TYANBOAT, Oxygen transport; Copper; Glycoprotein; Hemolymph.
INIT_MET_AL

170 170 COPPER I (BY SIMILARITY).
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01-WAR-1989 (Rel. 10, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
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 X-RAY CRYSTALLOGRAPHY (2.18 ANGSTROMS).

MEDLINE=93299372; PubMed=8518732;
Hazes B., Magnus K.A., Bonaventura C., Bonaventura J., Dauter Z.,
Kalk K.H., Hol W.G.J.;
"Crystal structure of deoxygenated Limulus polyphemus subunit II
hemocyanin at 2.18-A resolution: clues for a mechanism for allosteric
regulation.";
Protein Sci. 2:597-619(1993).
-!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS
OCCURRING FREELY DISSOLVED IN THE HEMOLYMEH OF MANY MOLLUSKS AND
                                                                   MEDLINE=91326804; PubNed=1866430; Magnus K.A., Lattman B.E., Volbeda A., Hol W.G.J.; Magnus K.A., Lattman B.E., Volbeda A., Hol W.G.J.; McGamers of subunit II from Limilus hemocyanin (a 48-mer) have the same quaternary structure as whole Panulirus hemocyanin molecules."; Proteins 9:240-247(1991).
        Yoketa E., Riggs A.F.; "The structure of the hemocyanin from the horseshoe crab, Limulus polyphemus. The amino acid sequence of the largest cyanogen bromide
                                                                                                                                                                                                               ARTHROPODS.
--- SUBUNIT: HEXAMER OR A MULTIPLE THEREOF.
--- SUBCELLULAR LOCATION: Extracellular.
--- TISSUE SPECIFICITY: Hemolymph.
--- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                                                                                                     R PDB; ILLA; DHRICAA.

R PDB; ILLA, 20-AUG-94.

R PDB; ILLA, 20-AUG-94.

R PDB; ILLA, 20-AUG-94.

R PDB; ILLA, 20-AUG-97.

R InterPro; IPR000896; Hemocyanin.

R InterPro; IPR005203; hemocyanin_C.

R InterPro; IPR005204; hemocyanin_C.

R InterPro; IPR005204; hemocyanin_C.

R Pfam; PF0372; hemocyanin_C; I.

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J. Biol. Chem. 259:4739-4749(1984).
MEDLINE=84185567; PubMed=6715319
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72628 MW; 6B8B4C6D8B1225BE CRC64;
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Search completed: December 16, 2003, 14:15:15 Job time : 5.66667 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Papinutto E., Dundon W.G., Pitulis N., Battistutta R., Montecucco C.,
Zanotti G.;
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97015126; PubMed=8861954; Takahashi M., Inoue N., Ohishi K., Maeda Y., Nakamura N., Endo Y., Fujita T., Takeda J., Kinoshita T.; Pita T. Takeda J., Kinoshita T.; Pita T. a membrane protein of the endoplasmic reticulum with a large lumenal domain, is involved in transferring the third mannose of the
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Babl, AR374269; AAM18636-1; -.
InterPro; IPR002177; DPS.
InterPro; IPR001519; Ferritin.
                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.3%; Score 45; DB 11; Length 542; 71.4%; Pred. No. 48; 1; Indels 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.8%; Score 44; DB 2; Length 147; 75.0%; Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBC, 15:4254-4261(1996),
EMBL, D84436; BAA94827.1; -.
MCD, MCI:1891825; Pigb.
InterPro; IPR005599; PMP.
Pfam; PF03901; PMP; 1.
SEQUENCE 542 AA; 63133 MW; OFCGBEBIDBAG67C1 CRC64;
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PROSITE; PS00818; DPS 1; 1.
SEQUENCE 147 AA; 16649 MW; 2741651884FCCCCD CRC64;
                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                            542 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                   Created)
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                                                         PRT;
                                                                                                             01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRRPQ1;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00210; ferritin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.07
Lace 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 HPWHWYL 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 HKWHWYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPI anchor."
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                                                            097760
   RESULT 2
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Dolichyl-phosphate-mannose--glycolipid alpha-mannosyltransferase-like
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                             White O., Bisen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.B., Salzberg S., Smith H.O., Venter J.C.,
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Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani
Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (AUG-2000) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.8%; Score 44; DB 16; Length 159; 62.5%; Pred. No. 21; Live 2; Mismatches 1; Indels
                                                                                                                                           Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, Al391149; CAC01884.1;
InterPro; IRR005599; PMP.
Pfam; PF03901; PMP; 1.
Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome.
SEQUENCE 159 AA; 17309 MW; FBGB9C87ED008F02 CRC64;
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                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein DR2142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498 AA.
 159 AA
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Arabidopsis thaliana (Mouse-ear cress).
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01-OCT-2000 (TrEMBLrel. 15, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last anno
                                     01-MAY-2000 (TrEMBLrel. 13, Created)
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PRT;
                                                                                                                                                                                                                                              MEDLINE=20036896; PubMed=10567266;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Science 286;1571-1577(1999).
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Matches 5; Conservative
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                           Deinococcus radiodurans.
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11 VHPWHWWV 18
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         radiodurans R1.";
                                                                                                                                                                               NCBI TaxID=1299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; DR2142; -.
                                                                                                                                                                                                                                                                                                                                                                    Fraser C.M.;
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                                                                                                        DR2142.
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 Q9RSI2
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Q9LEQ5
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68.8%; Score 44; DB 10; Length 498;

Query Match

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Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ECO17711; AAH17711.1; -.
Genew; HGNC:8959; PIGB.
                                                                                                                  InterPro; IPR005599; PMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                     306 HPWHWY 311
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                                                                                                                                                                                                                                                                                                           3 HKWHWY 8
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  TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPI anchor."
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Arsgi4850/T913 150.
Arsdidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Torlumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis ORF clones.",
"Arabidopsis ORF clones.",
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY120693; AAK91470.1; -.
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                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Koesena B., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P.,

Ranh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,

Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,

Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,

Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,

Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,

Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,

Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR005599; PMP.
Pfam; PF03901; PMP; 1.
SEQUENCE 548 Aa; 62701 MW; 125D3BEA0BF6A098 CRC64;
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Last annotation update)
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83.3%; Pred. No. 62;
ive 0; Mismatches
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01-MAR.2002 (TrEMBLrel. 20, Last seque
01-OCT-2002 (TrEMBLrel. 22, Last annot
Phosphatidylinositol glycan, class B.
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                           5; Conservative
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                  265 HPWHWY 270
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  Best Local Similarity
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SÉOUENCE FROM N.A.
                                                                     3 НКМНМУ 8
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                                                                                                                                                                                                                                     Q94A15
Q94A15;
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                           Matches
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Gaps
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MEDLINE=97015126; PubMed=8861954;
Takabashi M., Inoue N., Ohishi K., Maeda Y., Nakamura N., Endo Y.,
Tujita T., Takeda J., Kinoshita T.,
"Pujita T., a membrane protein of the endoplasmic reticulum with a large
lumenal domain, is involved in transferring the third mannose of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
                                                                                                                                                            .<del>.</del>
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.8%; Score 44; DB 4; Length 554; 83.3%; Pred. No. 69; live 0; Mismatches 1; Indels
                                                           Local Similarity 83.3%; Score 44; DB 4; Length 554; Local Similarity 83.3%; Pred. No. 69; Gonservative 0; Miamatchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO J. 15:4254-4261(1996).
EMBL: D42138; BAA07709.1; -.
InterPro: IPR005599; PMP.
Ffam: PF03901; PMP: B2AP87D13ADF90B3 CRC64;
PFdm; PF03901; PMP; 1.
PFdm; PF03901; PMP; 1.
SEOUENCE 554 AA; 64957 MW; E778418C02A27488 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
CG12006 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            561 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Page 4

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Gaps

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68.8%; Score 44; DB 5; Length 561; 83.3%; Pred. No. 70; ive 0; Mismatches 1; Indels

5; Conservative

Matches

Query Match Best Local Similarity

FlyBase; FBgn0035464; CG12006. InterPro; IRR005599; PMP. Pfam; PF03901; PMP; 1. SRQUENCE 561 AA; 65006 MW; 5A94054C6E9DB239 CRC64;

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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Braton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D.,
RA Abril J.F., Apdrews-Fennancoch C., Baldwin D.,
Ballew R.M., Basu A. Baxendale J., Bayraktaroglu L., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M.,
Beeson K.Y., Bence P.V., Bouck J., Brokesen P. Borlarer P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokesen P., Brotchar I.,
RA Borkova D., Botchan M., Buller H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Bolloher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Durbin K.J., Evangeliste C.C., Ferraz C., Ferrise S., Pielschmann W.,
RA Borlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Rocher C., Gabriellan A.B., Carg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeewam C.,
Alalin M., Ralush F., Karpen G.H., Ke Z., Kemison J., R.,
RA Harris B.E., Kodira C.D., Ferfat C., Morris J., Morsh D., Lais R.,
RA Liu X., Mattel B. McIntosh T.C., Morris J., Morsh D., Lais R.,
Rainer B.E., Kodira C.D., Reimen B.C., Siden K., Ban K.,
Rainer K., Ramingon K., Sannders R.D., Morsh D.M., Nelson D.L.,
Relson D.R., Nelson K., Sannders R.D., Smith T.,
Roue B.C., Siden Kiamos I., Simpson M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang S.,
RA Bang Z.-Y., Wasserman D.A., Weinschod W., Shoo V., Zho Q., Zho Y., Shen H.,
Ryirskas R., Tector C., Turner R., Venter E., Wang S., Zho Y., Shen H.,
Ryirskas R., Tector C., Turner R., Venter E., Wang S., Zho Y., Shen H.,
Ryirskas R., Tector C., Turner R., Venter E., Wang S., Zho Q., Zh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celniker S. B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y., Banzon J., An H., Baldwin D., Banzon J., Beeson K.T., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Boyle C., Dresnek D., Farfan D., Ferriera S., Frise E., Galle R.F., Mostin D., Howland T.U., A Gonzalez M., Hock J., Hoskins R.A., Hostin D., Howland T.C., Noy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Partel S., Pfeffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., A Williams S.M., Zaveri J. S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misra S., Croby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE003479; AAF47795.2; -.

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Asada N., Hatta T., Norioka S., Kawamoto N.;
"Properties activation and PCR-based sequence of prophenol oxidase A3
in Drosophila melanogaster."
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055857; BAB43866.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hyphantria cunea (Fall webworm).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.8%; Score 44; DB 5; Length 670; 62.5%; Pred. No. 82; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77493 MW; FF4A5D5CD4EE69C8 CRC64;
                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                      670 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 681 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; 1PR000896; Hemocyanin.
InterPro; 1PR005203; hemocyanin_C.
InterPro; 1PR005204; hemocyanin_N.
InterPro; 1PR005227; Tyrosinase.
Pfam; PP00372; hemocyanin; 1.
Pfam; PP00372; hemocyanin; 2, 1.
Pfam; PP03722; hemocyanin; 1.
Pfam; PR00372; hemocyanin; 1.
PR031TE; PR00187; HAEMOCYANIN.
PROSITE; PS00209; HEMOCYANIN_1; 1.
PROSITE; PS002109; HEMOCYANIN_1; 1.
PROSITE; PS00498; TYROSINASE_2; 1.
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                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                             Prophenol oxidase A3 (Fragment).
DOX-A3 OR DOX-3 OR CG2952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0000487; Dox-A3.
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                                                                                                                                                                                                                      PRELIMINARY;
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                                                            240 HPWHWY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              670 AA;
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3 HKWHWY 8
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                                                                                                                                                                                                                                                           Q9BLD9;
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                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                            Q9BLD9
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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Champe M., Charlin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Au C., Lewis S.E., Rubin G.M., Celniker S.,
Li Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AYOG1624; AAL29172.1; -..
RIVBASE; FEGNO000487; Dox-A3.
RIVERAPO; IPRO000869; Hemocyanin. C.
RITERPO; IPRO002207; Tyrosinse.
RinterPo; IPRO02227; Tyrosinse.
Ream; PPO3722; hemocyanin. C.
REAM; PFO3722; hemocyanin. C.
REAM; PFO3722; hemocyanin. C.
REAM; PFO3722; hemocyanin. C.
REAM; PFO3722; hemocyanin. C.
REAM; PRO01873; Hemocyanin. C.
REAM; PRO01872; Hemocyanin. C.
REAM; PRO01872; Hemocyanin. C.
REAM; PROSITE; PSO0210; HEMOCYANIN. 2; 1.
REAGIES; PSO0210; HEMOCYANIN. 2; 1.
REAGIES PSO0210; HEMOCYANIN. 2; 1.
REAGIES PSO0310; HEMOCYANIN. 2; 1.
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                                                                                                                                                             MEDLINE-98199915; PubMed-9537761;
Park D.S., Shin S.W., Kim M.G., Park S.S., Lee W.J., Brey P.T.,
Park H.Y.;
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Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.8%; Score 44; DB 5; Length 681; 62.5%; Pred. No. 84; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                       Pfam, PF00372; hemocyanin, 1.
Pfam, PF03722; hemocyanin, C: 1.
Pfam; PF03722; hemocyanin, N; 1.
PROSITE; PF001209; HEMOCYANIN, 1.
PROSITE; PF002109; HEMOCYANIN, 1; 1.
PROSITE; PF002109; HEMOCYANIN, 2; 1.
PROSITE; PF004989; TYROSINASE, 2; 1.
SEQUENCE 681 AA; 78195 MW; D85A513318312E83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 683 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR000896; Hemocyanin.
Interpro; IPR005203; hemocyanin C.
Interpro; IPR005204; hemocyanin N.
Interpro; IPR002277; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.8%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.5'
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
              Arctiidae, Hyphantria.
NCBI_TaxID=39466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 LHHWHWHL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LHKWHWYV 9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                              SEQUENCE FROM N.A.
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DOX-A3 OR CG2952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          095R43;
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Q95R43
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                   SOR BRANCO CREATER TO BRANCO CREATER AND BRANCO CRE
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RK STRAIN-BERKELEY;

RA Adams M.D., Celniker S.E., Holt R.A., Evvans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evvans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Lip P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Eichards S., Amburner W., Henderson S.N.,

Sutton G.G., Worthalb J.R., Yandell M.D., Zhang O., Chen L.K.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Bexter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Banu M., Barandale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Banu M.R., Bouck J., Bayraktaroglu L., Beasley E.M.,

Barkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,

RA Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,

RA Bortis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Plaischman W.,

RA Gloden R., Doup L.E., Downes M., Dugan-Rocha S., Ponkov B.C., Dunn P.,

RA Glodek A., Gong F., Gorrell J. H., Gu Z., Galbart W.M., Classer R.A.,

Adolf R., Harris M.L., Harren G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum R.A.,

Liu X., Mattei B., McIntosh T.C., McIeod M.P., McDerson D.L.,

RA Born D.K., Moy M., Murphy B., Murphy L., Murany D.M., Nelson D.L.,

Ra Born E.M., Moy M., R.A., Nikon K., Warisekar D.R., Paris K., Shen H.,

Ra Born E.K., Moy M., R., Nikon K., Warisekar D.K., Paris C., Stapleton M., Stupeki M.P., Smith T.,

Spier E., Spradling A.C., Pan S., Pollard J., Waissenbach J.,

Ra Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,

Ra Born E.K., Moyen F.W., Weinsenbach J., Wasserman D.A., Weinsenbach J.,

Rabon R.K., Moyen S.W., Wolson F.W., Weinsenbach J.,

Rabon R.K., Zhower S.W., Rollon W., Stupski M.P., Smith H.O.,

Rabon R.K., Zhower S.W., Rollon W., Stupski M.P., Smith H.O.,

Rabon R.K., Zhower S.W., Rollon W., Weinser D., Weinser P., Weinser P.W., Smith H.O.,

Rabon R.K., Zhower S.W., Rollon 
                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endotterygota; Diptera; Brachycera; Muscomorpha;
Pphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                683 AA.
                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13. Last sem
                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005203; hemocyanin C.
InterPro; IPR005204; hemocyanin N.
InterPro; IPR002227; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000896; Hemocyanin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF03723; hemocyanin_C; 1. PF03722; hemocyanin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003459; AAF46946.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00372; hemocyanin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :1yBase; FBqn0000487; Dox-A3.
                                                                                                                                                     PRELIMINARY;
                                       207 LHHWHWHL 214
2 LHKWHWYV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P04253; 10XY
                                                                                                                                                                                                                                                          CG2952 protein.
DOX-A3 OR CG2952.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li D.M., Schmidt O., Theopold U.;
"Insect hemocyte-derived microparticles are regulatory assemblages of the cell-derived immuse response.";
Submitted (JAN.2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF336289; AAK64363.1; -.
InterPro; IPR005895; Hemocyanin.
InterPro; IPR005203; hemocyanin. C.
InterPro; IPR005203; hemocyanin. N.
InterPro; IPR005227; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galleria mellonella (Wax moth).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Prerygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
NPyralidae; Galleriinae; Galleria.
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=7165;
                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                          Query Match 68.8%; Score 44; DB 5; Length 683; Best Local Similarity 62.5%; Pred. No. 84; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.8%; Score 44; DB 5; Length 683; 62.5%; Pred. No. 84; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00372; hemocyain; 1.
Pfam; PF03722; hemocyain, C; 1.
Pfam; PF03722; hemocyain, N; 1.
PROSTE; PF00187; HEMOCYANIN 1.
PROSTE; PS00210; HEMOCYANIN 1; 1.
PROSITE; PS00210; HEMOCYANIN 2; 1.
PROSITE; PS00498; TYROSINASE 2; 1.
SEQUENCE 683 AA; 78545 MW; 54AIF80F992839B7 CRC64;
PRINTS; PRO0187; HAEMOCYANIN.
PROSITE; PS00209; HEWOCYANIN 1; 1.
PROSITE; PS00210; HEMOCYANIN 2; 1.
PROSITE; PS00408; TYROSINASE 2; 1.
SEQUENCE 683 AA; 79314 MM; 437CBDD9E8A278BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Best Local Similarity 62.5:
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                    207 LHHWHWHL 214
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                                                                                                                                                                                                                                                                                                                        2 LHKWHWYV 9
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TISSUE=Body;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
2964D5
AC Q964D
AC Q964D
DT 01-DB
DT 01-MB
DT 0
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076951
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                                                                              Brey P.T.; "More and chromosomal localization of a prophenoloxidase "Molecular cloning and chromosomal localization of a prophenoloxidase CDNA from the malaria vector Anopheles gambiae."; Insect Mol. Biol. 7:41-50(1998)
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                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Ahmed A., Lee W.-J., Brey P.T., Ahmed A., Lee W.-J., Brey P.T., "Genomic structure of a prophenoloxidase from the malaria vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
MEDLINE=98119516; PubMed=9459428;
Lee W.J., Ahmed A., della Torre A., Kobayashi A., Ashida M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.8%; Score 44; DB 5; Length 683; larity 62.5%; Pred. No. 84; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF031826; AAD01936.1; --
RMBL; AF031826; AAD01936.1; --
RMBL; AF031826; AAD01936.1; --
HSSP; P04253; 10XT.
InterPro; IPR005203; hemocyanin.
InterPro; IPR005203; hemocyanin.
InterPro; IPR005227; Tyrosinase.
Ffam; PF0372; hemocyanin.
RFam; PF0372; 
                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 16, 2003, 14:18:01 Job time: 26 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 LHHWHWHL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
Les 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LHKWHWYV 9
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    a
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2003, 14:06:35; Search time 5.6667 Seconds (without alignments) 74.689 Million cell updates/sec

Title: US-09-870-089B-13 Perfect score: 55 Sequence: 1 KHFKPHGFS 9

Sequence: 1 KHFKPHGFS 9 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	) homo	17 mus m	vigr					Q9k0q4 neisseria m										Q24388 drosophila					_									3CW4	Q27536 caenorhabdi
ID	4 H	ATF4_MOUSE	PUR7_VIGAC	SAA HORSE	MB11 ARATH	Y4WF RHISN	NAGZ NEIMA	NAGZ_NEIMB	RL34_MYCPU	SODC_NEUCR	YBGL_ECOLI	RS31_ARATH		VE2 HPV52	BNA1 HUMAN	BNA1 RAT	HS70 PARBR	LSP2_DROME	MCE ASFB7	RL34 STAAM	YCSF BACSU	ACTR_CAVPO	PHOH_ECOLI	YNXO_YEAST	SPKA_SYNY3	SYV_VIBCH	PA2R BOVIN		ABH BACSU	LAMB EMENI	UBIG_RICCN	١.	GAL7_CAEEL
DB	: -	Н	Н	Н		-	-	Н	Н	Н	<b>~</b> 4		-	Н	Н	Н	Н	-4	~												٦		
Length	351	349	341	110	642	342	361	361	48	153	244	264	350	368	512	512	649	718	898	45	211	297	354	379	521	953	1463	2410	92	262	289	299	352
	100.0	89.1	σ	7	~	Ŋ	S	S	63.6	63.6	3	63.6	n	63.6	63.6	63.6	63.6	63.6	63.6	61.8		•		•			ä	Η.		Ö	60.0	٥.	ö
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Result No.	-	2	т	4	ις.	9	7	83	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q39473 cinnamomum Q9hfs2 cochliobolu	P55495 rhizobium s Q9wxr9 thermotoga	P51692 homo sapien P42232 mus musculu	P52632 rattus norv Q9tum3 bos taurus	Q9tuz0 sus scrofa 013797 homo sapien	O9h9y6 homo sapien
FATB_CINCA CREA_COCCA	Y4IL RHISN UXAC THEMA	STSB_HUMAN	STSB_RAT STSB_BOVIN	STSB_PIG	RPA2_HUMAN
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REDLINE=21016719; PubMed=11130712;

REDLINE=21016719; PubMed=11130712;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J. Attafi H., Araujo R., Bowman C.L., Brooks S.Y.,

R. Mile O., Alonso J., Altafi H., Cheuk R.F., Chin C.W.,

R. Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

R. Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Englis B.,

R. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

R. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

R. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

R. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

R. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

R. Hunter J.L., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

R. Hiltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

R. Ander S., Lee A., Lee J.M., Roney T., Rowley D.,

R. Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

R. Deterson J., Pham P.K., Rizzo M., Yosotskaia V.S., Walker M.,

R. Wu D., Yu G., Fraser C.M., Vaysberg M., Vysotskaia V.S., Walker M.,

R. Nu D., Yu G., Fraser C.M., Vaysberg M., Vysotskaia V.S., Walker M.,

R. Nu D., Yu G., Fraser C.M., Vaysberg M., Shinn R., Southwick A.M.,

R. Nu D., Yu G., Fraser C.M., Vaysberg M., Vysotskaia V.S., Walker M.,

R. Nu D., Yu G., Fraser C.M., Vaysberg M., Shinn R., Shinn R.,

R. Nu D., Yu G., Fraser C.M., Vaysberg M., Shinn R., Shinn R.,

R. Nu D., Yu G., Fraser C.M., Vaysberg M., Shinn R.,

R. Nu D., Yu G., Fraser C.M., Vaysberg M., Vocystkaia V.S., Walker M.,

R. Nu D., Yu G., Fraser C.M., Vaysberg M., Shinn R.,

R. Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Magnoliophyta; eudicotyledons; core eudicots; Rosidae,

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                              67.3%; Score 37; DB 1; Length 110;
83.3%; Pred. No. 4.8;
tive 1; Mismatches 0; Indels
                                                                                                                                                                     I -> L.
K -> Q.
G -> A.
FABTDBE7AB007E5B CRC64;
                         Nature 408:816-820(2000).
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Myrosinase binding protein-like Atlg52030.
ATIG52030 OR F5F19.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 642 AA.
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                                                                                                                                         1 60 ANY
16 16 16 I 4
44 44 K K
59 59 79 78 78 G 710 AA; 12289 MW; F
PRINTS; PR00306; SERUMAMYLOID
ProDom; PD002112; Serum amylo:
                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                 Local Similarity es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                2 HFKPHG 7
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                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                       VARIANT
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MB11_ARATH
ID MB11 A
                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-00T-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-hexosaminidase (RC 3.2.1.52) (N-acetyl-beta-glucosaminidase)
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InterPro, IPR002103; Bac luciferase.
Fam, PF00296; bac luciferase, 1.
Hypothetical procein; Oxidoreductase; Monooxygenase; Plasmid.
SEQUENCE 342 AA; 37665 MW; EBID57A71EDA8953 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid sym pNGR234a.
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae, Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Beta-N-acetylhexosaminidase).
NAGZ OR NMADONG.
Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                               Match 67.3%; Score 37; DB 1; Length 642;
Local Similarity 85.7%; Pred; No. 27;
Local Similarity 85.7%; Pred; No. 27;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 55.5%; Score 36; DB 1; Length 342; Similarity 75.0%; Pred. No. 22; onservative 0; Mismatches 2; Indels 6; Conservative 0; Mismatches 2; Indels
Pfam; PF01419; Jācalin; 4.
Bectin; Repeat; Miltispene family.
SEQUENCE 642 AA; 68849 WW; 9ABOBS69A6SC913C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypotherical 37,7 kDa protein Y4NF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 342 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                            157 KHPKPQG 163
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                        F RHISN
Y4WF RHISN
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                                                                                                                      Query Match
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Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Grazlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                Science 287:1809-1815(2000).

-!- FUNCTION: Cleaves GlcNAc linked beta-1,4 to MurNAc tripeptides
-!- FUN similarity).

-!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-
-!- PATHWAY: Call wall synthesis, murein tripeptide recycling pathway.
-!- SUBCELLINIAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLINIAR: DELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES. NAGZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galisson F.,
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Nucleic Acids Res. 29:2145-2153(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; WF_00364; -; 1.
InterPro; IPR01764; Glyco_hydro_3N.
Pfam; PF00933; Glyco_hydro_3; J.
Pfam; PF00975; GLYCOSTL_HYDROL. F3; FALSE_NEG.
Hydrolase; Glycosidase; Peptidoglýcan synthesis; Cell division;
Cell wall; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.5%; Score 36; DB 1; Length 361; 75.0%; Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
3E066E5B9809033A CRC64;
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Last annotation update)
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0; Mismatches
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16-OCT-2001 (Rel. 40, Last sequ
28-FBB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AA; 39152 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-acetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides.
-!- PATHWAY: Call wall synthesis, murain tripeptide recycling pathway.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR: BELONGS TO FAMILY 3 OF GLYCOSYL HYDROLASES. NAGZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MCS8 / Serogroup B, MEDLINE=2017575; PubMed=10710307; Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
                                                                                                          PERGINE 22491 / Serogroup A / Serotype 4A;

MEDLINE 2022556; PubMed=10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Rate S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Mhitchead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                      Nature 404:502-506(2000).
-!- FUNCTION: Cleaves GlCNAc linked beta-1,4 to MurNAc tripeptides (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-hexosaminidase (RC 3.2.1.52) (N-acetyl-beta-glucosaminidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF 00364; -; 1.
InterPro; IPR001764; Glyco_hydro_3N.
Pfam; PF00333; Glyco_hydro_3; D.
PROSITE; PS00775; GLYCOSYL_HYDROL_F3; FALSE_NEG.
Hydrolase; Glycosidase; Peptidoglycan synthesis; Cell division; Cell wall; Complete proteome.

ACT SITE 258 258 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.5%; Score 36; DB 1; Length 361; 75.0%; Pred. No. 23; 2; Indels tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174F048B59CAAFBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL162754; CAB83994.1; -. PIR; H81913; H81913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 AA; 39022 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-N-acetylhexosaminidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 75.0 les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                   Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 KHFPGHGF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KHFKPHGF 8
                                                                                                                                                                                                                                                                                                                                              meningitidis 22491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                         SEQUENCE FROM N.A.
                                        NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAGZ OR NMB0530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAGZ NEIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09K004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAGZ NEIMB
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Gaps

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurospora crassa.";
J. Biol. Chem. 260:9559-9566(1985).

-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.

-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).

-!- COPACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE=91035418; PubMed=2146266;
Chary P., Hallewell R.A., Natvig D.O.;
Structure, exon pattern, and chromosome mapping of the gene for "Structure, exon pattern, and chromosome mapping of the gene for cytosolic copper-zinc superoxide dismutase (sod-1) from Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBUNIT: Homodimer.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lerch K., Schenk E.;
"Primary structure of copper-zinc superoxide dismutase from
                                                                                                                                                                                                                                                                                                                                       Score 35; DB 1; Length 48; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                  MYDULIST: MYDUSOMAI L34.

INTERPROPOSE RIDOSOMAI L34; I.

PEGNIN: PROFOSE RIDOSOMAI L34; I.

TIGREAMS: TIGRO1030; rpmH bact; I.

PROSITE: PROFOSE; RESOSOMAL L34; I.

PROSITE: PROFOSE; RESOSOMAL L34; I.

RIDOSOMAI PYCLEIN; COMPLETE PYCLEOME.

SEQUENCE 48 AA; 5581 MW; 72F420BD6EC4DD43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1988 (Rel. 07, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Deproxide dismutase [Cu-Zn] (EC 1.15.1.1).
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 265:18961-18967(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=85261356; PubMed=3160699;
                                                                                                    EMBL; AL445563; CAC13327.1; -.
                                                                                                                                                                                                                                                                                                                                         63.6%;
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 KHAKTHGF 19
                                                                                                                                                                                                                                                                                                                                                                                                                   1 KHFKPHGF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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EMBL; M58687; AAA63780.1; -.

PIR; A36591; A36591.

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99420866; PubMed=10493123;
Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
"Enrichment of low abundance proteins of Escherichia coli by hydroxyapatite chromatography.";
Electrophoresis 20:2181-2195(1999).
-!- SIMILARITY: STRONG, TO H.INFLUENZAE H11729.
                                                                                                                                                                                                                                                       0;
                                                                                                            COPPER (BY SIMILARITY).
COPPER AND ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
                                                                                                                                                                                                                               DB 1; Length 153;
                                     ProDom; PD000469; SOD CUZN.1; 1.
PROSITE; PS00087; SOD_CUZN.1; 1.
PROSITE; PS00332; SOD_CUZN.2; 1.
PROSITE; PS00332; SOD_CUZN.2; 1.
INIT MET 0.
METAL 46 46 COPPER (RV SIMILEDITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                              T -> A (IN REF. 2).
56DAFAC86CD9573B CRC64;
                                                                                                    COPPER (BY SIMILARITY).
                                                                                                                                                                       COPPER (BY SIMILARITY)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                               Score 35; DB
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3]
IDENTIFICATION BY MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
        InterPro; IPR001424; SOD_CU_ZN.
Pfam; PF00080; sodcu; 1.
PRINTS; PR00068; CUZNDISMTASE.
                                                                                                  63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                          153 AA;
                                                                                                                                                                                                                               Query Match
Best Local Similarity
HSSP; P00445; 1JCV
                                                                                                                                                                                                                                                                                                    63 HFNPHG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             2 HFKPHG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                       Protein ybgh.
                                                                                                                                                                                                                                                                                                                                                              (BGL ECOLI
                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                    METAL
                                                                                                                           METAL
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us-09-870-089b-13.rsp

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T51304; T51304.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KHFKPHG 7
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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RS40 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            datches
  SOLUTION DE REPRESENTANT DE RE
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Salanoubat M., Lemcker, R. Rieger M., Perez-Alonso M., Obermaier B.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
A Delseny W., Choisne N., Artiguenave F., Robert C., Brottier P.,
R. Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
A Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
R. Schaefer M., Dragole M., Pallavicini A., Toppo S., Simionari B.,
R. Vezzi A., Dragole M., Pallavicini A., Toppo S., Simionari B.,
R. Vezzi A., Dragole M., Schoen O., Bargues M., Terol J., Climent J.,
R. Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
R. Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
R. Navaro P., Collado C., Perez-Perez A., Ottenwaelder B., Masuy D.,
de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
Monfort A., Argintou A., Flores M., Liguori R., Vitale D.,
Monfort A., Argintou A., Flores M., Liguori R., Vitale D.,
Monfort A., Argintou A., Flores M., Liguori R., Vitale D.,
Mayer K.R.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lopato S., Waigmann E., Barta A.; "Characterization of a novel arginine/serine-rich splicing factor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P92954, 0944A4; Q9M278;
15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginine/serine-rich splicing factor RSP31.
Arginine/serine-rich splicing factor RSP31.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
-!- SIMILARITY: TO B.NIDULANS LACTAM UTILIZATION PROTEIN LAMB AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 63.6%; Score 35; DB 1; Length 244; Best Local Similarity 71.4%; Pred. No. 24; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 AA; 25800 MW; DBC0FD14ADA0EB0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=97143875; PubMed=8989882;
                                                                                                                                                                                                                                                                                                                                             EcoGene; EG13308; VbgL.
InterPro; IPR005501; Lamb_YcsF.
Pfam; PF0346; Lamb_YcsF.
Complete proteome.
SEQUENCE 244 AA; 25800 MW: n
                                                                                                                                                                                                                                                                             EMBL; AE000174; AAC73807.1; -.
EMBL; D90710; BAA35377.1; -.
PIR; H64806; H64806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Cell 8:2255-2264(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                           B.SUBTILIS YCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 RHVKPHG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KHFKPHG 7
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RS31 ARATH
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Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S., Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V., Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu B., Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanaba A., Yamada M., Yasuda M., Tabata S.; Saguence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
-:- SIMILARITY: BELOWGS TO THE SR FAMILY OF SPLICING FACTORS.
-:- CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Nuclear (Potential).
-1- TISSUE SPECIFICITY: Highly expressed in roots and flowers. A presumably longer alternatively spliced form is found in leaves, stems and flowers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
WIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
SSP consortium (Salk/Stranford/PGEC) ";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: REQUIRED FOR CONSTITUTIVE AND ALTERNATIVE PRE-MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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PROSITE, PSSO102; RRW, 2.
PROSITE, PSO0JO, RRW RNP 1, FALSE NEG.
PROSITE, PSO0JO, RRW RNP 1, FALSE NEG.
Nuclear protein, RNA-binding, Alternative splicing, Repeat.
74 RNA-BINDING (RRM) 1.
74 RNA-BINDING (RRM) 2.
164 FNA-BINDING (RRM) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.6%; Score 35; DB 1; Length 264; 71.4%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARG/SER-RICH (RS DOMAIN).
R -> K (IN REF. 1).
445FDZE4A5E0C203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R840_ARATH STANDARD; PRT; 350 AA. P92965; Q96333; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Arginine/serine-rich splicing factor RSP40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 26;
2; Mismatches
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EMBL; AF439831; AAL27502.1; -.
EMBL; AX125565; AAM78075.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P09651, 1HA1.
InterPro; IPR000637; AT hook.
InterPro; IPR000504; RNA_rec_mot.
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264 AA; 31154 MW;
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                                                                                                                                                                                                                                                                                                                                                                                               Nature 408:820-822(2000).
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SMART; SM00360; RRM; 2.
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SOLUTION DESCRIPTION DE LA PRIME DEL PRIME DE LA PRIME DEL PRIME DE LA PRIME D
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                               Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Vuridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Rosidae,
Surantophyta, Massicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                      Lopato S., Waigmann E., Barta A.; "Characterization of a novel arginine/serine-rich splicing factor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
Wintz H., Sakamoto W.;
submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
MEDLINE=97143875; PubMed=8989882;
   RSP40 OR AT4G25500 OR M7J2.130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant Cell 8:2255-2264(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barta A.
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                                                                                                                                                                                                                                                                                                                            the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Delius H., Hofmann B.;

"Primer-directed sequencing of human papillomavirus types.";

Curr. Top. Microbiol. Immunol. 186:13-31(1994).

-!- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

-!- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

IT BINDS TO THE SEXE RESPONSE ELEMENT (5'-ACCINNININGGT-3') PRESENT

IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN ETTHER

ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION

WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS

BY STERICALLY HINDERING THE ASSENBLY OF THE TRANSCRIPTION

INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                         -!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: Highly expressed in roots and flowers. A presumably longer alternatively spliced form is found in leaves.
               -!- FUNCTION: REQUIRED FOR CONSTITUTIVE AND ALTERNATIVE PRE-MRNA SPLICING (BY SIMILARITY).
                                                                                                                                                                                        -!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muclear protein; RNA-binding; Alternative splicing; Repeat.

DOMAIN 2 74

RNA-BINDING (RRM) 1.

DOMAIN 97 168

RNA-BINDING (RRM) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 1; Length 350;
Pred. No. 34;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4A1C779BB94B32A6 CRC64;
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K -> R (IN REF. 3).

R -> T (IN REF. 3).

S -> T (IN REF. 3).
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; 19700504; RNA_rec_mot.
Pfam; PF00076; rrm; 2.
SNARY; SM00360, RRM; 2.
PROSITE; PS01022; RRM; 2.
PROSITE; PS01030; RRM RNP_1; FALSE_NEG.
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MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X99437; CAA67800.1; -.
EMBL; U76607; AAB18813.1; -.
EMBL; AL022197; CAA18176.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 63.6%;
Similarity 71.4%;
5; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168
350
27
27
66
195
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Best Local Similarity
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P36796;
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VE2_HPV52
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                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         016515; Q13553;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Amiloride-sensitive brain sodium channel BNaCl (Amiloride-sensitive
cation channel neuronal 1) (BNCl) (Degenerin channel MDEG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "BNaCl and BNaC2 constitute a new family of human neuronal sodium channels related to degenerins and epithelial sodium channels."; Proc. Natl. Acad. Sci. U.S.A. 94:1459-1464(1997).
                                                                                                                                                                                                                                                                                                          PIR, 266576; S36576.

HNSP; PIT383; IDPM.

InterPro; IPR000427; E2 C.

InterPro; IPR001866; E2 N.

Pfam; PF00511; E2 C; 1.

Probom; PF00508; E2 N; 1.

Probom; PD000672; E2 C; 1.

Probom; PD000673; E2 N; 1.

Barly protein; Transcription; Activator; DNA-binding; Trans-acting factor; DNA replication; Repressor; Nuclear protein. SEQUENCE 368 AA; 41739 MW; 32128423B2F629D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garcia-Anoveros J., Derfler B.H., Neville-Golden J., Hyman B.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.6%; Score 35; DB 1; Length 368; 55.6%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 271:10433-10436(1996).
                       -!- SUBUNIT: Binds DNA as a dimer.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Frontal cortex;
MEDLINE=97188490; PubMed=9037075;
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                                                                                                                                                                                                                                                                                        EMBL; X74481; CAA52588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 KYFKKHGYT 116
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  REPLICATION
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MEDLINE=21661460; PubMed=11802773;
MEDLINE=21661460; PubMed=11802773;
Hruska-Hageman A.M., Wemmis J.A., Price M.P., Welsh M.J.;
Hruska-Hageman A.M., Wemmis J.A., Price M.P., Welsh M.J.;
Hruska-Hageman A.M., Wemmis J.A., Price M.P., Welsh M.J.;
Kinase I) with the non-voltage gated sodium channels BNCI (brain Na-channel I) and ASIC (acid-sensing ion channel).";
Biochem. J. 361:443-450(2002).
-1- FUNCTION: Non-voltage-gated amiloride-sensitive cation channel permeable for sodium, potassium and lithium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 601784; -. G.integral to plasma membrane; TAS. GO; 0005887; C.integral to plasma membrane; TAS. GO; 00105280; F.amiloride-sensitive sodium channel activity; TAS. GO; GO:0007417; P.central nervous system development; TAS. GO; GO:0007422; P.peripheral nervous system development; TAS. GO; GO:0007268; P.synaptic transmission; TAS.
                                                                                                                                                                                                                                   permeable for sodium, potassium and lithium.
--- SUBUNIT: Interacts with PRKCABP.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: BRAIN AND SPINAL CORD.
--- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
T -> A [IN REF. 2).
7C95B0B32EFF2814 CRC64;
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR004724; EnaC.
Interpro; IPR001873; Na+channel_ASC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1078; AMINACHANNEL.
TIGRFAMS; TIGR00859; ENAC; 1.
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EMBL; U50352; AAC50432.1; -.
EMBL; U57352; AAB49182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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512
365
392
495
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495
512 AA;
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Search completed: December 16, 2003, 14:15:17 Job time: 6.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: December 16, 2003, 14:06:35; Search time 5.66667 Seconds (without alignments) 74.689 Million cell updates/sec

Title: US-09-870-089B-13 Perfect score: 55 Sequence: 1 KHFKPHGFS 9 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	P18848 homo sapien	mus m	Q07463 vigna aconi	P19857 equus cabal	-		Q9jvt3 neisseria m		Q98r56 mycoplasma	P07509 neurospora		4						Q24388 drosophila		Q99qt1 staphylococ		Q9zls9 cavia porce		P53861 saccharomyc		Q9kp73 vibrio chol				P38096 emericella		7W.4	-
SUMMARIES		ID	ATF4 HUMAN	ATF4 MOUSE	PUR7 VIGAC		MB11 ARATH	Y4WF RHISN	NAGZ NEIMA	NAGZ_NEIMB	RL34_MYCPU	SODC_NEUCR	YBGL_ECOLI	RS31_ARATH	RS40_ARATH	VE2 HPV52	BNA1_HUMAN	BNA1_RAT	HS70_PARBR	LSP2_DROME	MCE ASFB7	RL34 STAAM	YCSF_BACSU	ACTR_CAVPO	PHOH_ECOLI		SPKA_SYNY3	SYV_VIBCH			ABH BACSU				GAL7_CAEEL
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	Ouerv	'	100.0	89.1	69.1	67.3	67.3	65.5	65.5	65.5	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	61.8											•	0.09	•
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Q39473 cinnamomum	Q9hfs2 cochliobolu	P55495 rhizobium s	Q9wxr9 thermotoga	092gll rickettsia	P51692 homo sapien	P42232 mus musculu	P52632 rattus norv	Q9tum3 bos taurus	Q9tuz0 sus scrofa	Q13797 homo sapien	Q9h9y6 homo sapien
FATB_CINCA	CREA COCCA	Y41L RHISN	UXAC_THEMA	SYGB RICCN	STSB_HUMAN	STSB_MOUSE	STSB RAT	STSB_BOVIN	STSB_PIG	ITA9 HUMAN	RPA2_HUMAN
-1	-	7	-	<del>, -</del> 1		-	+4	+-4	٦	-	7
382	430	432	451	670	786	786	786	787	787	1035	1079
0.09	0.09	0.09	0.09	0.09	0.09	60.09	60.09	60.09	0.09	60.09	0.09
33	33	33	33	33	33	33	33	33	33	33	33
34	35	36	37	38	39	40	47	42	43	44	45

## ALIGNMENTS

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RESULT.

TO 1-804-1900 (Rel. 16, Created)

TO 1-804-1900 (Rel. 15, Lear and Lotter out of the following by the following protein TARKEB67) (Cyclic Amplement Figure 1 (Cyclic Amplement Figure 1 (MAN-binding protein TARKEB67) (Cyclic Amplement Figure 2 (MAN-binding protein William Stock MAN-Binding William Stock MAN-Binding Protein William Stock MAN-Binding Protein William Stock MAN-Binding Protein William Stock MAN-Binding WAN-Binding WAN-Bindin
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Minoshima S., Kawasali K., Sasaki T., Patkwa S., Wodoh J.,

R. Minoshima S., Kawasali K., Yoshima S., Wodoh J.,

R. Mana S., Chen Y., Say C., L. Catherre J., Deschumes S., Do A., Do T.,

R. Documan A., Chan Y., Min P., Will M., Manida S., Wayen T., Ban H.,

R. Documan A., Chan Y., Min P., Will M., Manida S., Wayen T., Ban H.,

R. Documan A., Chan Y., Min P., Will M., Walla S., Wayen T., Ban H.,

R. Documan A., Mang G., Chan Y., Ray L., Ran O., Shauli S., Slaan D., Song L.,

R. Documan A., Mang G., Chan Y., Ray L., Ran O., Shauli S., Slaan D., Song L.,

R. Documan A., Mang G., Minson S., Minte D., Willingham D., Wayen T., Ban H.,

R. Documan A., Mang G., Chan Song S., Minte D., Willingham D., Wayen T., Banking D.,

R. Documan A., Mang G., Land S., Shan M., Watter S., Waterston R., Wilson R.,

R. Documan H., S., Dibmoon R., Mong A.C.C., Morrow B.E., Edudari M., L.,

R. Schee P., Waller C., Wanghey A., Wohldaman P., Peppin K., Wallson R.,

R. Milliagon D., Boddenteich A., Manida E., Materston R., Wilson R.,

R. Williagon D., Boddenteich A., Martman K., Hu X., Khan A.S., Lane L.,

R. Milliagon D., Boddenteich A., Martman K., Hu X., Khan A.S., Lane L.,

R. Milliagon D., Boddenteich A., Martman K., Hu X., Khan A.S., Lane L.,

R. Marsener R.D., Colling F.S., Magner L., Schmenn C.M., Schuler G.D.,

R. Marsener R.D., Colling F.S., Magner L., Schmen C.M., Galbe R. R.,

R. Marsener R.D., Colling F.S., Magner L., Schmen C.R., Schuler G.D.,

R. Marsener R.D., Colling F.S., Magner L., Schwen R.D., Williago S.,

R. Milliagon M., Marsulia M., Watter M.A., Marse M.A.,

R. Marsener R.D., Colling F.S., Magner L., Shanker R.D., Ghillengthe S.,

R. Marsener R.D., Colling F.S., Magner L., Shanker R.D., Ghillengthe S.,

R. Marsener R.D., Colling F.S., Magner L., Shanker R.D., Min M. M.,

R. Marsener R.D., Colling F.S., Magner L., Shanker R.D., Min M.,

R. Marsener R.D., Colling F.S., Magner L., Shanker R.D., Min M.,

R. Marsener R.D., Colling F.S., Magner L., Shanker R.D.,

R. Marsener R.D., Colling F.S., Magner L., Shanker S.D.,

R.
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Q06507; Q61906;

Q01-PEB-1996 (Rel. 33, Created)

Q1-FEB-1996 (Rel. 33, Last sequence update)

Z8-FEB-2003 (Rel. 41, Last annotation update)

Cyclic-AMP-dependent transcription factor ATF-4 (C/EBP-related ATF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB=Adipocyte;

PUBDLINE=281642; PubMed=8506317;

Vallejo M., For D., Miller C.P., Habener J.F.;

"C/ATF, a member of the activating transcription factor family of DNA-binding proteins, dimerizes with CAATF, enhancer-binding proteins and directs their binding to CAMP response elements."; Proc. Natl. Acad. Sci. US.A. 90:4679-4683(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Protein interaction cloning in yeast: identification of mammalian proteins that react with the leucine zipper of Unn."; Proc. Natl. Acad. Sci. U.S.A. 89:5789-5793(1392).
-i- FUNCTION: BINDS TO ASYMMETRIC CAMP RESPONSE ELEMENTS (CRE) AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 55; DB 1; Length 351; 100.0%; Pred. No. 0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                  F -> Q (IN REF. 3).

K -> R (IN REF. 2).

T -> R (IN REF. 2).

K I -> REW (IN REF. 5).

K I -> L (IN REF. 5).

X 7A708CSCCD6ED7F8 CRC64;
                                                                                                                                                                                                                                                                               LEUCINE-ZIPPER (PROBÁBLE).
E -> D (in dbSNP:1803324).
/FTId=VAR 014768.
                                                                                                                                       MIM; 604064; -. GO:0003677; F:DNA binding activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                    BASIC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAINS-CD-1, TISSUE-Embryo;
MEDLINE=92335183; PubMed=1631061;
Chevray P.M., Nathans D.;
                                 AL022312; CAB45284.1; -. BC008090; AAH08090.1; -. BC011994; AAH11994.1; -. BC024775; AAH24775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      38558 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
            EMBL; D90209; BAA14234.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (C/ATF) (TAXREB67 homolog).
                                                                                                                                                                                                                                                         3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                      M86842; AAA52071.
                                                                                                                        HGNC: 786; ATF4.
                                                                                                 PDB; 1CI6; 04-DEC-00.
TRANSPAC; T01303; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 KHFKPHGFS 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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284 2
290 2
329 3
338 3
                                                                                     PIR; A45377; A45377
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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ATF4 MOUSE
                       EMBL;
EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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